# A microsatellite-based linkage map for song sparrows (Melospiza melodia)

Nietlisbach, Pirmin ; Camenisch, Glauco ; Bucher, Thomas ; Slate, Jon ; Keller, Lukas F ; Postma, Erik

Abstract: Although linkage maps are important tools in evolutionary biology, their availability for wild populations is limited. The population of song sparrows ( Melospiza melodia) on Mandarte Island, Canada, is among the more intensively studied wild animal populations. Its long-term pedigree data, together with extensive genetic sampling, have allowed the study of a range of questions in evolutionary biology and ecology. However, the availability of genetic markers has been limited. We here describe 191 new microsatellite loci, including 160 high-quality polymorphic autosomal, 7 Z-linked and 1 W-linked markers. We used these markers to construct a linkage map for song sparrows with a total sex-averaged map length of 1731 cM and covering 35 linkage groups, and hence, these markers cover most of the 38–40 chromosomes. Female and male map lengths did not differ significantly. We then bioinformatically mapped these loci to the zebra finch ( Taeniopygia guttata) genome and found that linkage groups were conserved between song sparrows and zebra finches. Compared to the zebra finch, marker order within small linkage groups was well conserved, whereas the larger linkage groups showed some intrachromosomal rearrangements. Finally, we show that as expected, recombination frequency between linked loci explained the majority of variation in gametic phase disequilibrium. Yet, there was substantial overlap in gametic phase disequilibrium between pairs of linked and unlinked loci. Given that the microsatellites described here lie on 35 of the 38–40 chromosomes, these markers will be useful for studies in this species, as well as for comparative genomics studies with other species.

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# A microsatellite-based linkage map for song sparrows (*Melospiza melodia*)

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**Table S1:** Locus characteristics for 209 autosomal markers (chr=A), of which 160 are of high quality and used for the linkage map (sel=1), 2 are W-linked (chr=W), 8 are Z-linked (chr=Z), and one is a sex-diagnostic locus (chr=ZW). Most markers are previously unpublished, except for the following: Escμ001 (developed for reed bunting, *Emberiza schoeniclus*) from Hanotte *et al.* (1994); Gf005 (developed for medium ground finch, *Geospiza fortis*) from Petren (1998); Mme001, Mme002, Mme007, Mme008, and Mme012 (developed for song sparrow) from Jefferey *et al.* (2001); Sosp01, Sosp02, Sosp03, Sosp04, Sosp05, Sosp07, Sosp08, Sosp10, Sosp12, Sosp13, and Sosp14 (developed for song sparrow) from Sardell *et al.* (2010). CHD is used for sex determination and its primers were modified by Hoeck *et al.* (2009) based on sequences generated by primers P2 and P8 from Griffith *et al.* (1998). This table is sorted according to these columns: chr, sel, panel, marker.

| marker | sel | chr | rep | forward primer | reverse primer | pc | panel | $T_A$ | cyc | $N_1$ | pr | $N_2$ | $N_A$ | range | $H_O$ | $H_E$ | $H_E/H_O$ | drop | false | GenBank |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Sosp004 | 1 | A | 4 | gtttcGGTTGATGGGGATGTTTCTG | FAM_CTTCTTGAGCTTGGGGTCAC | 0.05 | 1 | 60 | 28 | 3258 | 1.00 | 3249 | 8 | 182-222 | 0.62 | 0.62 | 1.01 | 0.0002 | 0.0001 | GU301258 |
| Sosp005 | 1 | A | 4 | gtttcGAAGGTGTTGGTGCTCACAG | FAM_CTCCTGGGCCAGACAAAG | 0.044 | 1 | 60 | 28 | 3261 | 1.00 | 3245 | 6 | 112-132 | 0.65 | 0.70 | 1.08 | 0.0007 | 0.0001 | GU301259 |
| Sosp007 | 1 | A | 4 | gtttcGTTCCGAGCCCATCCATCT | PET_CTCTGAGCCCTGCGTTGT | 0.02 | 1 | 60 | 28 | 3215 | 0.99 | 3157 | 4 | 95-107 | 0.55 | 0.56 | 1.01 | 0.0254 | 0.0009 | GU301261 |
| Sosp008 | 1 | A | 4 | gtttcGTCCTTGGAGTTTGCAGGTATC | VIC_CCTGCAAAAGTAAGAAAGAGAGG | 0.024 | 1 | 60 | 28 | 3234 | 0.99 | 3216 | 5 | 174-186 | 0.14 | 0.13 | 0.99 | 0.0010 | 0.0001 | GU301262 |
| Sosp014 | 1 | A | 4 | gtttcGGGCTTTCTGGCAAAGATATG | NED_AAAAAGGGGCTTAGGTCCAG | 0.066 | 1 | 60 | 28 | 3244 | 0.99 | 2954 | 12 | 224-276 | 0.70 | 0.72 | 1.02 | 0.0106 | 0.0298 | GU301268 |
| Escμ001 | 1 | A | 2 | VIC_TTCTCTTGGTCTATGGAAGGTG | gtttcGCTTGAAAGACAGTCACCAGG | 0.034 | 3 | 57 | 28 | 3216 | 0.99 | 3205 | 9 | 133-153 | 0.78 | 0.77 | 0.99 | 0.0001 | 0.0006 | X77077 |
| Mme002 | 1 | A | 2 | FAM_ATCAGAGATTCCTGCTACACACCC | gtttcGAAATTGTATCCGCCACCTCATTC | 0.2 | 3 | 57 | 28 | 3261 | 1.00 | 3258 | 16 | 123-175 | 0.80 | 0.80 | 1.00 | 0.0001 | 0.0001 | AF127377 |
| Mme008 | 1 | A | 2 | gttTCATGGAGATGGGTGAATGCC | VIC_TGAATCAGCAGCACACACAACC | 0.028 | 3 | 57 | 28 | 3259 | 1.00 | 3224 | 9 | 207-226 | 0.84 | 0.84 | 0.99 | 0.0017 | 0.0001 | AF127382 |
| Sosp013 | 1 | A | 4 | PET_AGGGAGGAGGCAGAAAATGT | gtttcGAGGTGTTTTTCGCTGATTTG | 0.036 | 3 | 57 | 28 | 3259 | 1.00 | 3185 | 11 | 187-231 | 0.77 | 0.78 | 1.01 | 0.0022 | 0.0160 | GU301267 |
| Mme012 | 1 | A | 6 | gtttcAGGGACTGTCACTGTGGGACTGAAG | PET_TGGCTTTATGGAACAAGGCATC | 0.04 | 5 | 64 | 28 | 3259 | 1.00 | 3250 | 10 | 187-246 | 0.54 | 0.54 | 1.00 | 0.0002 | 0.0004 | AF127385 |
| Sosp001 | 1 | A | 4 | gtttcGCCAACACCCTCAACAAGAT | FAM_ACCAACTGATGCACCTTCTG | 0.1 | 5 | 64 | 28 | 3255 | 1.00 | 3235 | 14 | 207-286 | 0.80 | 0.82 | 1.02 | 0.0009 | 0.0019 | GU301255 |
| Sosp002 | 1 | A | 4 | gtttcAAACTCGCGTCTTTGCTAGG | VIC_CAGGTGTCCTGCAGATGTTG | 0.05 | 5 | 64 | 28 | 3255 | 1.00 | 3253 | 4 | 165-177 | 0.72 | 0.72 | 1.00 | 0.0005 | 0.0002 | GU301256 |
| Sosp010 | 1 | A | 4 | NED_TCCCCTGTGGAAGTTGTCTC | gtttcGTCCACAGAGCAGTCACAGAGG | 0.034 | 5 | 64 | 28 | 3240 | 0.99 | 3238 | 5 | 167-187 | 0.64 | 0.64 | 1.00 | 0.0008 | 0.0001 | GU301264 |
| Sosp017 | 1 | A | 2 | FAM_AGACCTGCTCTTCAGGTGGA | gtttcGCTGCCTCCAAAAAGATGAG | 0.14 | 6 | 59 | 28 | 2425 | 0.98 | 2425 | 7 | 230-243 | 0.75 | 0.74 | 0.98 | 0.0001 | 0.0001 | KP998210 |
| Sosp029 | 1 | A | 3 | FAM_GCCAAGGCTGTCAGAGTTTC | gtttcGGCTCTGTGATTTTCCTGCT | 0.1 | 6 | 59 | 28 | 2411 | 0.98 | 2370 | 15 | 167-212 | 0.77 | 0.77 | 1.00 | 0.0073 | 0.0283 | KP998211 |
| Sosp030 | 1 | A | 2 | PET_ACACTGGCTGTTCTCTGCCT | gtttcGGAAGTTCAGGTTGCCAAAA | 0.1 | 6 | 59 | 28 | 2312 | 0.94 | 2305 | 11 | 134-156 | 0.82 | 0.83 | 1.01 | 0.0006 | 0.0011 | KP998212 |
| Sosp033 | 1 | A | 2 | PET_GAATGGCAGTCACACCACAC | gtttcGAGCTCCCACACTACCCAGA | 0.18 | 6 | 59 | 28 | 2414 | 0.98 | 2226 | 15 | 183-288 | 0.82 | 0.83 | 1.02 | 0.0199 | 0.0011 | KP998213 |
| Sosp035 | 1 | A | 2 | PET_TCCATCTTTGCAGCACTGAC | gtttCGGCTATTTCAGGGTGATTC | 0.28 | 6 | 59 | 28 | 2338 | 0.95 | 2270 | 12 | 381-412 | 0.67 | 0.67 | 1.01 | 0.0040 | 0.0110 | KP998214 |
| Sosp047 | 1 | A | 4 | FAM_CAGTCAGAATCCAGTCTGCAA | gtttcTGCTGACCATGTCACACCTT | 0.4 | 6 | 59 | 28 | 2169 | 0.88 | 2084 | 20 | 402-456 | 0.76 | 0.77 | 1.02 | 0.0003 | 0.0206 | KP998215 |
| Sosp062 | 1 | A | 4 | FAM_CCCCAATACTCCCAAATCCT | gtttcGCAACTGGAAGATGGCTACAG | 0.4 | 6 | 59 | 28 | 2341 | 0.95 | 2293 | 15 | 341-395 | 0.87 | 0.88 | 1.01 | 0.0001 | 0.0217 | KP998216 |
| Sosp142 | 1 | A | 2 | VIC_CAACGTTCAGCCTAAAGGGA | gtttcAAGGAGATTTTGCCTGTTGC | 0.08 | 6 | 59 | 28 | 2369 | 0.96 | 2369 | 3 | 379-383 | 0.51 | 0.54 | 1.06 | 0.0003 | 0.0001 | KP998217 |
| Sosp043 | 1 | A | 2 | VIC_GGGTCATTCAACAGGCACTT | gtttcACTGGACCAGCCAGCTAGAA | 0.04 | 8 | 59 | 28 | 2310 | 0.94 | 2301 | 7 | 277-296 | 0.81 | 0.83 | 1.02 | 0.0001 | 0.0019 | KP998218 |
| Sosp050 | 1 | A | 3 | NED_CTGCTCTCTCCTTCCCTGTG | gttTCCAGTAGTGGAATCCAGGC | 0.08 | 8 | 59 | 28 | 2246 | 0.91 | 2199 | 20 | 394-472 | 0.88 | 0.89 | 1.01 | 0.0001 | 0.0047 | KP998219 |
| Sosp054 | 1 | A | 2 | VIC_CAGCATGTTCCACTCTCCAG | gtttcTTACCTGACCAGGGTTCTCG | 0.1 | 8 | 59 | 28 | 2340 | 0.95 | 2330 | 13 | 370-406 | 0.76 | 0.75 | 0.99 | 0.0001 | 0.0028 | KP998220 |
| Sosp061 | 1 | A | 3 | PET_GGCAAGTGCTTTTCTTTTGC | gtttCTGGAAATGCCTTGGGACTA | 0.1 | 8 | 59 | 28 | 2361 | 0.96 | 2279 | 17 | 155-211 | 0.85 | 0.85 | 1.00 | 0.0006 | 0.0016 | KP998221 |

| marker | sel | chr | rep | forward primer | reverse primer | pc | panel | $T_A$ | cyc | $N_1$ | pr | $N_2$ | $N_A$ | range | $H_O$ | $H_E$ | $H_E/H_O$ | drop | false | GenBank |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Sosp068 | 1 | A | 5 | FAM_GAGCACCTGTGCTGCTTACA | gtttcTATCTGCTGCTGTGGAATGC | 0.1 | 8 | 59 | 28 | 2249 | 0.91 | 2059 | 21 | 391-446 | 0.81 | 0.83 | 1.02 | 0.0119 | 0.0281 | KP998222 |
| Sosp037 | 1 | A | 4 | VIC_AGCAAAGGATTCTCCCCATT | gtttcTTGTCCCCCAAGTCTTTCAG | 0.04 | 9 | 59 | 28 | 2083 | 0.84 | 2080 | 5 | 262-270 | 0.72 | 0.73 | 1.00 | 0.0002 | 0.0009 | KP998223 |
| Sosp049 | 1 | A | 2 | NED_AGCTCATCAGCAGCTCCAAT | gtttCTGACACCCATCAGGTGCT | 0.08 | 9 | 59 | 28 | 2353 | 0.95 | 2353 | 3 | 163-171 | 0.64 | 0.66 | 1.02 | 0.0002 | 0.0002 | KP998224 |
| Sosp055 | 1 | A | 4 | FAM_ACCTTTGTATGCAGAGGGCA | gttTCACAGGAACAAAGGGGAAG | 0.08 | 9 | 59 | 28 | 2348 | 0.95 | 2042 | 10 | 394-426 | 0.74 | 0.79 | 1.06 | 0.0311 | 0.0177 | KP998225 |
| Sosp076 | 1 | A | 3 | PET_CCAGTGGTGTCCCAAGAGTT | gtttCTGCTCAGGGAGTGAAAGGT | 0.22 | 9 | 59 | 28 | 2318 | 0.94 | 2310 | 16 | 371-447 | 0.82 | 0.82 | 1.00 | 0.0001 | 0.0001 | KP998226 |
| Sosp003 | 1 | A | 4 | PET_CACCTGGTTTCAGTTAGGTTCC | gtttcAAGGGGCTGACCCAAGGT | 0.08 | 10 | 59 | 28 | 2417 | 0.98 | 2391 | 15 | 186-248 | 0.86 | 0.89 | 1.03 | 0.0011 | 0.0032 | GU301257 |
| Sosp052 | 1 | A | 4 | FAM_TAAACCATGCTTGGAAGGCT | gtttcAGGACACAGGGGAAAAAGGT | 0.06 | 10 | 59 | 28 | 2372 | 0.96 | 2241 | 9 | 201-253 | 0.74 | 0.77 | 1.05 | 0.0198 | 0.0025 | KP998227 |
| Sosp065 | 1 | A | 3 | NED_ACTCCCCAAATCCCTGACAC | gtttcGTTGGCAAGTTGGTGTTGTG | 0.04 | 10 | 59 | 28 | 2378 | 0.96 | 2347 | 11 | 171-204 | 0.71 | 0.70 | 0.99 | 0.0002 | 0.0026 | KP998228 |
| Sosp069 | 1 | A | 2 | PET_GGAGGGAAGAGAAAGTTGGG | gtttCTTTGCCTCCACTAAATGGC | 0.04 | 10 | 59 | 28 | 2396 | 0.97 | 2390 | 7 | 280-294 | 0.76 | 0.73 | 0.97 | 0.0002 | 0.0001 | KP998229 |
| Sosp070 | 1 | A | 2 | PET_GAAATTTGGCCAGGAGATGA | gtttcAACTCCACTGCTCTGGGAGA | 0.08 | 10 | 59 | 28 | 2316 | 0.94 | 2221 | 5 | 444-456 | 0.43 | 0.43 | 1.01 | 0.0020 | 0.0001 | KP998230 |
| Sosp012 | 1 | A | 4 | FAM_CACTGTGCTTTTCATAGGCAAC | gtttcGAAAAACGATGGAGCAAAGC | 0.1 | 11 | 60 | 28 | 2342 | 0.95 | 2273 | 11 | 141-176 | 0.78 | 0.80 | 1.03 | 0.0004 | 0.0359 | GU301266 |
| Sosp022 | 1 | A | 4 | VIC_GATTTCCCCCTCTGCTCTTC | gtttcGGTGCTTCTCCTCAGATTGG | 0.04 | 11 | 60 | 28 | 2383 | 0.97 | 2379 | 12 | 98-147 | 0.87 | 0.87 | 1.00 | 0.0001 | 0.0001 | KP998231 |
| Sosp025 | 1 | A | 2 | VIC_CAATGACCACACCAGCAAAC | gtttcTGGGAGACAGTGGAAAAAGC | 0.04 | 11 | 60 | 28 | 2354 | 0.95 | 2351 | 11 | 389-424 | 0.79 | 0.80 | 1.02 | 0.0001 | 0.0001 | KP998232 |
| Sosp018 | 1 | A | 2 | NED_AGGAAGCTGGTCAGGCTGTA | gtTTCTCCCCATTCCCTTCTCT | 0.04 | 12 | 60 | 28 | 2346 | 0.95 | 2337 | 7 | 114-164 | 0.54 | 0.54 | 1.01 | 0.0002 | 0.0001 | KP998233 |
| Sosp024 | 1 | A | 2 | FAM_GCAACATGTGCTCTGTGCTT | gttTCTCAGGACAGTAAGGGTTGC | 0.2 | 12 | 60 | 28 | 2424 | 0.98 | 2369 | 14 | 110-168 | 0.75 | 0.76 | 1.01 | 0.0113 | 0.0006 | KP998234 |
| Sosp041 | 1 | A | 2 | PET_TGTGCCTGGTCTTGTGACAG | gtttcACAGGACACCCTTTGGTCTG | 0.1 | 12 | 60 | 28 | 2362 | 0.96 | 2300 | 8 | 413-436 | 0.62 | 0.62 | 1.00 | 0.0072 | 0.0023 | KP998235 |
| Sosp056 | 1 | A | 2 | VIC_ACAGGACATGCACCATTTCA | gtttCCAAGGCTAGTTTCTGCCTG | 0.04 | 12 | 60 | 28 | 2385 | 0.97 | 2385 | 5 | 118-128 | 0.56 | 0.56 | 1.00 | 0.0003 | 0.0001 | KP998236 |
| Gf005 | 1 | A | 2 | FAM_AAACACTGGGAGTGAAGTCT | gtttcAACTATTCTGTGATCCTGTTACAC | 0.5 | 13 | 58 | 32 | 2070 | 0.84 | 2033 | 15 | 191-243 | 0.87 | 0.86 | 0.99 | 0.0043 | 0.0008 | AF081929 |
| Sosp141 | 1 | A | 4 | FAM_TGTGCTGCCTGTGTTCTTTT | gtttcGAAGTTTCCCCTTGCCCTAC | 0.2 | 13 | 58 | 32 | 2367 | 0.96 | 2357 | 6 | 292-305 | 0.64 | 0.65 | 1.01 | 0.0026 | 0.0001 | KP998237 |
| sosp_ng007 | 1 | A | 2 | FAM_TGGAAATCCTACCAACCTGG | gtttcTGCTCTGCTGTTGATGATCC | 0.1 | 15 | 60 | 25 | 2416 | 0.98 | 2405 | 3 | 96-100 | 0.55 | 0.52 | 0.96 | 0.0022 | 0.0002 | KP998238 |
| sosp_ng082 | 1 | A | 5 | NED_TCCACACCAACAGAGTTCCA | gtttCACGGAGGAAGTACCAGGAG | 0.16 | 15 | 60 | 25 | 2396 | 0.97 | 2213 | 15 | 115-205 | 0.81 | 0.82 | 1.02 | 0.0401 | 0.0013 | KP998239 |
| sosp_ng083 | 1 | A | 2 | FAM_AATGCCACTTTCACCTCCAG | gtttCTCAGCACCTCCCTCACAAT | 0.1 | 15 | 60 | 25 | 2425 | 0.98 | 2395 | 9 | 160-185 | 0.27 | 0.26 | 0.99 | 0.0085 | 0.0175 | KP998240 |
| sosp_ng142 | 1 | A | 2 | VIC_CTGTTCTCTTGGGCATCCAG | gtttcGTCATTGGAGAGGTGGCACT | 0.06 | 15 | 60 | 25 | 2404 | 0.97 | 2395 | 5 | 214-229 | 0.32 | 0.32 | 1.01 | 0.0007 | 0.0025 | KP998241 |
| sosp_ng149 | 1 | A | 4 | NED_GTCTGCAGGAGACAAGGACC | gtttcAGGGCAGGAGTAAGCAGACA | 0.16 | 15 | 60 | 25 | 2403 | 0.97 | 2390 | 11 | 215-258 | 0.79 | 0.80 | 1.02 | 0.0022 | 0.0020 | KP998242 |
| sosp_ng154 | 1 | A | 4 | FAM_CGGGCATTTATCCCTGAGT | gtttcAGCAGATTTAGCGGCTTGAA | 0.2 | 15 | 60 | 25 | 2281 | 0.92 | 2178 | 6 | 229-245 | 0.64 | 0.66 | 1.03 | 0.0125 | 0.0006 | KP998243 |
| sosp_ng001 | 1 | A | 2 | PET_TTTCCATGCTCTCCTGCTTC | gtttcGGAATAACACTGGGCTCTGC | 0.1 | 16 | 60 | 25 | 2374 | 0.96 | 2355 | 5 | 86-96 | 0.75 | 0.75 | 1.01 | 0.0002 | 0.0001 | KP998244 |
| sosp_ng012 | 1 | A | 2 | FAM_CCAAGGCATTTCCTCAGAAG | gtttcAGCACAAACCCATAGCAACC | 0.34 | 16 | 60 | 25 | 2382 | 0.96 | 2371 | 6 | 98-108 | 0.63 | 0.62 | 0.99 | 0.0002 | 0.0001 | KP998245 |
| sosp_ng055 | 1 | A | 2 | VIC_ACAGGCAAAGACACCTTGCT | gtttcGGAGGCGAGACAGATCAAGA | 0.06 | 16 | 60 | 25 | 2396 | 0.97 | 2207 | 7 | 131-143 | 0.71 | 0.74 | 1.04 | 0.0362 | 0.0001 | KP998246 |
| sosp_ng091 | 1 | A | 4 | PET_GACAGGCAGGAGATGAAAGC | gtttcTTGATGGGAGGTGGCTAAAG | 0.04 | 16 | 60 | 25 | 2392 | 0.97 | 2392 | 3 | 167-175 | 0.31 | 0.32 | 1.03 | 0.0004 | 0.0001 | KP998247 |
| sosp_ng113 | 1 | A | 2 | VIC_GAGCCAGACATTCAGAAGGG | gtttcGTGCCGTGGCCTAGTACAGT | 0.04 | 16 | 60 | 25 | 2387 | 0.97 | 2384 | 10 | 180-201 | 0.66 | 0.65 | 0.99 | 0.0002 | 0.0001 | KP998248 |
| sosp_ng159 | 1 | A | 4 | NED_CAGATGTTTCTGCAGGGCTT | gtttcATGAACCTTGTTGGCTCCAC | 0.2 | 16 | 60 | 25 | 2362 | 0.96 | 2329 | 16 | 202-363 | 0.89 | 0.91 | 1.02 | 0.0006 | 0.0060 | KP998249 |
| sosp_ng002 | 1 | A | 2 | NED_TAGTGCTGTTGGGAATGCAG | gtttcTGTGATGGATCTGTTTGGGTT | 0.06 | 17 | 60 | 25 | 2370 | 0.96 | 2364 | 3 | 86-95 | 0.50 | 0.49 | 0.98 | 0.0003 | 0.0002 | KP998250 |
| sosp_ng033 | 1 | A | 2 | VIC_CCACTCAGTCTGCCTGTCAA | gtttcTATCCTCGTTTGCCACACTG | 0.06 | 17 | 60 | 25 | 2371 | 0.96 | 2359 | 5 | 113-125 | 0.70 | 0.71 | 1.01 | 0.0002 | 0.0001 | KP998251 |
| sosp_ng048 | 1 | A | 4 | PET_GTCCTTGAGGCATGGTGTTT | gtttcGCCAGGAGCTTGTTCTCATC | 0.34 | 17 | 60 | 25 | 2126 | 0.86 | 2120 | 8 | 99-145 | 0.76 | 0.75 | 0.99 | 0.0007 | 0.0001 | KP998252 |
| sosp_ng109 | 1 | A | 4 | PET_GGGAAATGGACAGCTCACAG | gttTCCTCAAGTTGTTGGCAAAG | 0.06 | 17 | 60 | 25 | 2361 | 0.96 | 2361 | 3 | 192-200 | 0.12 | 0.11 | 0.97 | 0.0012 | 0.0001 | KP998253 |
| sosp_ng123 | 1 | A | 4 | NED_GGAGGGTCAGATTTGGGTCT | gttTCCTTCTCCACAGAGCTGGT | 0.06 | 17 | 60 | 25 | 2343 | 0.95 | 2330 | 11 | 144-218 | 0.67 | 0.66 | 0.98 | 0.0010 | 0.0012 | KP998254 |
| sosp_ng173 | 1 | A | 4 | PET_GTCAGCCCGATGAGACAAAT | gtttcGCAGCATTGCTAAAGGCTTG | 0.3 | 17 | 60 | 25 | 2252 | 0.91 | 2245 | 5 | 256-276 | 0.72 | 0.70 | 0.98 | 0.0002 | 0.0001 | KP998255 |
| sosp_ng004 | 1 | A | 2 | FAM_AGTTCTGCCATGAACAAGCC | gtttCGTTTCTCGATGTCCTCGTA | 0.14 | 18 | 60 | 25 | 2232 | 0.90 | 2232 | 10 | 75-96 | 0.49 | 0.48 | 0.99 | 0.0003 | 0.0001 | KP998256 |

| marker | sel | chr | rep | forward primer | reverse primer | pc | panel | $T_A$ | cyc | $N_1$ | pr | $N_2$ | $N_A$ | range | $H_O$ | $H_E$ | $H_E/H_O$ | drop | false | GenBank |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| sosp_ng006 | 1 | A | 6 | PET_CAGTCAAGAGGAGAGGCAGC | gtttcTTTGTGCCTGTGTCAGCAGT | 0.1 | 18 | 60 | 25 | 2257 | 0.91 | 2254 | 8 | 87-136 | 0.47 | 0.47 | 0.99 | 0.0003 | 0.0001 | KP998257 |
| sosp_ng072 | 1 | A | 2 | NED_TTTCTGGAAACAAACCCACC | gtttcTAATTGGGAAATGGACACCC | 0.1 | 18 | 60 | 25 | 2212 | 0.90 | 2209 | 6 | 138-149 | 0.60 | 0.63 | 1.06 | 0.0002 | 0.0001 | KP998258 |
| sosp_ng119 | 1 | A | 2 | NED_CCTGATGGGCTGCAATAGTT | gttTCTGCCATTCAGTCAGCAAC | 0.08 | 18 | 60 | 25 | 2166 | 0.88 | 2124 | 3 | 199-203 | 0.46 | 0.46 | 0.99 | 0.0016 | 0.0002 | KP998259 |
| sosp_ng120 | 1 | A | 4 | PET_TCTTCTGCAACATGACCTTGA | gtttcGCAGTACAAGCCAGTGGGAT | 0.2 | 18 | 60 | 25 | 2224 | 0.90 | 2185 | 6 | 201-221 | 0.57 | 0.59 | 1.04 | 0.0120 | 0.0001 | KP998260 |
| sosp_ng126 | 1 | A | 5 | FAM_TTGCAGATGGGACTGAGACA | gtttCAGTGTCTGTGCAGGTCCAG | 0.2 | 18 | 60 | 25 | 2229 | 0.90 | 2211 | 18 | 146-229 | 0.89 | 0.90 | 1.02 | 0.0001 | 0.0047 | KP998261 |
| sosp_ng200 | 1 | A | 5 | FAM_GATTGATGGCCACAAACCTC | gttTCACCTTCCTCTCCTCCTTG | 0.2 | 18 | 60 | 25 | 2214 | 0.90 | 2214 | 13 | 275-335 | 0.81 | 0.79 | 0.98 | 0.0001 | 0.0001 | KP998262 |
| sosp_ng053 | 1 | A | 5 | VIC_TCCCTCCTGTTATCCCTGTG | gtTTCTCCTTTCCAGCAGGATG | 0.06 | 19 | 60 | 25 | 2351 | 0.95 | 2344 | 4 | 117-132 | 0.38 | 0.40 | 1.07 | 0.0031 | 0.0001 | KP998263 |
| sosp_ng081 | 1 | A | 5 | FAM_TGTCCAGAGGAAGGGCTATG | gtttcAATGCAAAGGTAGGGACGTG | 0.1 | 19 | 60 | 25 | 2350 | 0.95 | 2334 | 9 | 137-185 | 0.73 | 0.75 | 1.02 | 0.0001 | 0.0025 | KP998264 |
| sosp_ng086 | 1 | A | 5 | PET_GGGCTGAAGGAGGTCACATA | gtTTCCCAAGCTGCAGTAGGTC | 0.06 | 19 | 60 | 25 | 2335 | 0.95 | 2305 | 12 | 151-194 | 0.76 | 0.74 | 0.96 | 0.0008 | 0.0007 | KP998265 |
| sosp_ng134 | 1 | A | 4 | FAM_CCTATGGTGACACTCCAGCA | gtttcGTTACACCCGACAAGGCTGT | 0.1 | 19 | 60 | 25 | 2341 | 0.95 | 2339 | 2 | 215-219 | 0.50 | 0.50 | 0.99 | 0.0003 | 0.0014 | KP998266 |
| sosp_ng161 | 1 | A | 4 | PET_TCTGCCATGTAAGAACACGC | gtttCCGTTTCCATCGTATTCCTG | 0.2 | 19 | 60 | 25 | 2307 | 0.93 | 2279 | 4 | 235-243 | 0.23 | 0.24 | 1.03 | 0.0007 | 0.0001 | KP998267 |
| sosp_ng197 | 1 | A | 4 | FAM_GTATCACATGCTGGGAGGCT | gtttcGACAGGTGGAGCACAGCAC | 0.2 | 19 | 60 | 25 | 2315 | 0.94 | 2298 | 19 | 269-367 | 0.81 | 0.82 | 1.02 | 0.0042 | 0.0001 | KP998268 |
| sosp_ng054 | 1 | A | 5 | NED_AGAAGCTGCGTGCCTCTTAG | gtttCACGAGTTTGAAGCTGTGGA | 0.08 | 20 | 60 | 25 | 2343 | 0.95 | 2268 | 16 | 129-210 | 0.80 | 0.80 | 1.01 | 0.0007 | 0.0371 | KP998269 |
| sosp_ng132 | 1 | A | 4 | VIC_TTTCAGTTCAGCCAGGCTTT | gtttcAAGGCTTGGTTTGGTCTCCT | 0.06 | 20 | 60 | 25 | 2394 | 0.97 | 2394 | 2 | 209-213 | 0.36 | 0.35 | 0.98 | 0.0005 | 0.0002 | KP998270 |
| sosp_ng137 | 1 | A | 4 | PET_TGATCCCAAATCTTGGCTTT | gtttcGGGTTTGGGAGGGAAGTTT | 0.2 | 20 | 60 | 25 | 2387 | 0.97 | 2376 | 9 | 198-242 | 0.79 | 0.79 | 1.00 | 0.0006 | 0.0006 | KP998271 |
| sosp_ng163 | 1 | A | 2 | FAM_GGAGGATGACATGGGAGAAA | gtttcGCTGAGGCTGCCAGATCTAC | 0.34 | 20 | 60 | 25 | 2197 | 0.89 | 2194 | 8 | 242-256 | 0.70 | 0.69 | 0.99 | 0.0002 | 0.0006 | KP998272 |
| sosp_ng172 | 1 | A | 5 | VIC_GCAGTCAGACTAGAGGAGCGA | gtttcTTGTTGGGTAACAGGCATCA | 0.1 | 20 | 60 | 25 | 2380 | 0.96 | 2352 | 11 | 246-296 | 0.87 | 0.87 | 1.00 | 0.0001 | 0.0021 | KP998273 |
| sosp_ng037 | 1 | A | 4 | FAM_ACAGCTCATTCCTGGCTGAT | gtttcTTTGATTGCAGGGATGATGA | 0.16 | 21 | 60 | 25 | 2411 | 0.98 | 2362 | 7 | 117-141 | 0.71 | 0.72 | 1.01 | 0.0002 | 0.0012 | KP998274 |
| sosp_ng045 | 1 | A | 2 | NED_AGCCAGACTGCACAATCTCA | gtttCCTGCCTTTCCAAATCTCAC | 0.12 | 21 | 60 | 25 | 2425 | 0.98 | 2421 | 4 | 130-138 | 0.39 | 0.37 | 0.97 | 0.0003 | 0.0012 | KP998275 |
| sosp_ng058 | 1 | A | 4 | VIC_GGAAAGGCCGAGTCACTGTA | gtttCCTCACAGCCATGAGAGTCA | 0.2 | 21 | 60 | 25 | 2415 | 0.98 | 2376 | 7 | 110-153 | 0.78 | 0.78 | 1.01 | 0.0006 | 0.0006 | KP998276 |
| sosp_ng096 | 1 | A | 4 | FAM_TCTTGGGATGAATTTGGAGC | gtttcAAACCAAACAGGAATGCAGC | 0.1 | 21 | 60 | 25 | 2446 | 0.99 | 2446 | 4 | 176-188 | 0.13 | 0.13 | 1.01 | 0.0017 | 0.0001 | KP998277 |
| sosp_ng107 | 1 | A | 2 | VIC_ATTGCACCATGCTCACTCAG | gtttcACAGCAATCAGGAGTCAGGC | 0.16 | 21 | 60 | 25 | 2437 | 0.99 | 2437 | 5 | 189-197 | 0.66 | 0.67 | 1.00 | 0.0002 | 0.0001 | KP998278 |
| sosp_ng146 | 1 | A | 6 | NED_CATGAAACGCTGCCTACAAA | gttTCAATCTGGCACAGCGTTAG | 0.2 | 21 | 60 | 25 | 2413 | 0.98 | 2362 | 18 | 193-288 | 0.83 | 0.81 | 0.98 | 0.0001 | 0.0048 | KP998279 |
| sosp_ng008 | 1 | A | 4 | PET_AGAGCCTGCGTGTTCTTCAT | gtttcGAGAAATGGGCTGTCCACAT | 0.06 | 22 | 60 | 25 | 2431 | 0.98 | 2292 | 11 | 87-131 | 0.85 | 0.86 | 1.01 | 0.0315 | 0.0006 | KP998280 |
| sosp_ng034 | 1 | A | 4 | FAM_GACAGTCAACCAAGGCAGGT | gtttcGCCTGAAGCTCCATGCTAAC | 0.04 | 22 | 60 | 25 | 2437 | 0.99 | 2429 | 12 | 116-167 | 0.67 | 0.69 | 1.02 | 0.0002 | 0.0001 | KP998281 |
| sosp_ng098 | 1 | A | 2 | NED_TTGCAGCCTCCTCTTTGTCT | gtttcAGGAGGAGAATTGGAGCGAT | 0.1 | 22 | 60 | 25 | 2380 | 0.96 | 2274 | 18 | 178-351 | 0.69 | 0.69 | 1.00 | 0.0002 | 0.0251 | KP998282 |
| sosp_ng115 | 1 | A | 2 | PET_TGTAGATGTCCGTCTGCTGC | gttTCCAGGACTTCTGTGTGCTG | 0.04 | 22 | 60 | 25 | 2448 | 0.99 | 2448 | 3 | 191-199 | 0.15 | 0.15 | 0.98 | 0.0010 | 0.0001 | KP998283 |
| sosp_ng128 | 1 | A | 2 | FAM_TGCCAGAAGTGTTGTCAAGC | gtttCCCTAATTCAGCTGTGGAGG | 0.1 | 22 | 60 | 25 | 2432 | 0.99 | 2408 | 11 | 203-233 | 0.67 | 0.66 | 0.99 | 0.0002 | 0.0010 | KP998284 |
| sosp_ng160 | 1 | A | 4 | PET_TGTTCTCAGCTGCTGTCTGG | gtttcGAGCGTGGACAAATCCAAAT | 0.24 | 22 | 60 | 25 | 2318 | 0.94 | 2318 | 3 | 240-248 | 0.50 | 0.50 | 1.01 | 0.0003 | 0.0001 | KP998285 |
| sosp_ng194 | 1 | A | 2 | FAM_GGATCACCTTCAGCCAGACT | gtttcGCCACATGTGCACTCAAGAT | 0.2 | 22 | 60 | 25 | 2383 | 0.97 | 2254 | 8 | 284-304 | 0.73 | 0.73 | 1.01 | 0.0180 | 0.0409 | KP998286 |
| sosp_ng071 | 1 | A | 4 | FAM_CCTTTCTGTAGGCTTGGCTG | gtttCTGGAGATGAAAGCAAAGGG | 0.1 | 23 | 59 | 25 | 2457 | 1.00 | 2424 | 12 | 134-173 | 0.88 | 0.88 | 0.99 | 0.0001 | 0.0022 | KP998287 |
| sosp_ng088 | 1 | A | 5 | NED_TCTGATGTGCTGGGCTACTG | gtttcGGTTCTTGTCCTCCCACAGA | 0.14 | 23 | 59 | 25 | 2442 | 0.99 | 2283 | 12 | 148-208 | 0.78 | 0.78 | 1.01 | 0.0139 | 0.0001 | KP998288 |
| sosp_ng206 | 1 | A | 5 | VIC_CCCTGATTCCAGCAAAGTATG | gtttcGAGAATCCATTTCTGCCCAA | 0.04 | 23 | 59 | 25 | 2460 | 1.00 | 2443 | 6 | 126-151 | 0.76 | 0.78 | 1.03 | 0.0012 | 0.0007 | KP998289 |
| sosp_ng247 | 1 | A | 4 | NED_GGTACCAGAGCTGCTCCTCA | gtttcGTTCTCAGCTCAGGCCAAAC | 0.04 | 23 | 59 | 25 | 2456 | 0.99 | 2456 | 3 | 88-96 | 0.59 | 0.60 | 1.02 | 0.0002 | 0.0001 | KP998290 |
| sosp_ng334 | 1 | A | 3 | VIC_CCTTCCTGTGAGGATGTGGT | gtttcACCTCCATGGGACACCAG | 0.16 | 23 | 59 | 25 | 2461 | 1.00 | 2461 | 2 | 242-245 | 0.47 | 0.47 | 1.00 | 0.0003 | 0.0002 | KP998291 |
| sosp_ng351 | 1 | A | 3 | VIC_CGTGCAAGGTTAAGAGGAGC | gtttcAGATCCACTTCTGCACACCC | 0.04 | 23 | 59 | 25 | 2464 | 1.00 | 2464 | 3 | 189-198 | 0.26 | 0.26 | 1.01 | 0.0007 | 0.0001 | KP998292 |
| sosp_ng219 | 1 | A | 4 | PET_AAGCCACCTGCTTTCAGAGA | gtttCGTGCAGGGCTCTTCTTTAT | 0.04 | 24 | 59 | 25 | 2459 | 1.00 | 2456 | 9 | 93-129 | 0.71 | 0.73 | 1.04 | 0.0001 | 0.0005 | KP998293 |
| sosp_ng239 | 1 | A | 5 | NED_GGGAAGATTGATCGGGATAC | gtttCCGCAGAGCTGAAATAAAGG | 0.08 | 24 | 59 | 25 | 2462 | 1.00 | 2462 | 8 | 121-161 | 0.37 | 0.37 | 1.00 | 0.0004 | 0.0001 | KP998294 |

| marker | sel | chr | rep | forward primer | reverse primer | pc | panel | $T_A$ | cyc | $N_1$ | pr | $N_2$ | $N_A$ | range | $H_O$ | $H_E$ | $H_E/H_O$ | drop | false | GenBank |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| sosp_ng256 | 1 | A | 2 | VIC_AGAGCACATTATGTTCCCGC | gttTCTAGACGGTTGTACCTGCTG | 0.04 | 24 | 59 | 25 | 2452 | 0.99 | 2274 | 7 | 111-125 | 0.59 | 0.63 | 1.06 | 0.0223 | 0.0228 | KP998295 |
| sosp_ng269 | 1 | A | 4 | PET_GTCACATTCCGTGGGATAGC | gtttcATGCATGGATACCAACCACA | 0.2 | 24 | 59 | 25 | 2462 | 1.00 | 2350 | 10 | 184-220 | 0.78 | 0.79 | 1.01 | 0.0392 | 0.0057 | KP998296 |
| sosp_ng343 | 1 | A | 3 | NED_TGCACCCTTTAATCCCTTTG | gttTCAACTCAAGGCTCAACTTCC | 0.04 | 24 | 59 | 25 | 2459 | 1.00 | 2459 | 4 | 205-216 | 0.51 | 0.50 | 0.98 | 0.0003 | 0.0001 | KP998297 |
| sosp_ng358 | 1 | A | 3 | VIC_TCAGCTACCTGGGCCTTCTA | gtttcAGAGATTCACTGCACCGGAC | 0.04 | 24 | 59 | 25 | 2466 | 1.00 | 2466 | 3 | 191-197 | 0.22 | 0.21 | 0.96 | 0.0005 | 0.0001 | KP998298 |
| sosp_ng385 | 1 | A | 3 | VIC_GGTTCTCTGTGCAGCCGT | gtttcGGGAAGCAGAGTATGACCCA | 0.06 | 24 | 59 | 25 | 2359 | 0.96 | 2249 | 7 | 268-297 | 0.45 | 0.46 | 1.02 | 0.0224 | 0.0039 | KP998299 |
| sosp_ng392 | 1 | A | 2 | PET_CAGGTATTAAAGGACAGGACCA | gtttCTGGATTTGCAGCTGTTTCA | 0.08 | 24 | 59 | 25 | 2453 | 0.99 | 2444 | 5 | 277-287 | 0.64 | 0.64 | 1.00 | 0.0002 | 0.0001 | KP998300 |
| sosp_ng215 | 1 | A | 4 | NED_TCAGGACCTTGTCAAAGGCT | gtttcTGGAGTGACTGCATCAATGG | 0.04 | 25 | 59 | 25 | 2459 | 1.00 | 2454 | 6 | 94-114 | 0.71 | 0.69 | 0.97 | 0.0001 | 0.0001 | KP998301 |
| sosp_ng238 | 1 | A | 4 | FAM_CACAATTCCTCTGCTCCCAT | gtttCTTGCCAAAGTCCAGCTGTT | 0.3 | 25 | 59 | 25 | 2450 | 0.99 | 2397 | 18 | 93-187 | 0.87 | 0.87 | 1.00 | 0.0006 | 0.0081 | KP998302 |
| sosp_ng279 | 1 | A | 5 | NED_TTGTTGGTGAACTGCTCAGG | gtttCTGGGACAGTGGAGGTGAG | 0.04 | 25 | 59 | 25 | 2458 | 1.00 | 2447 | 14 | 175-239 | 0.77 | 0.77 | 1.00 | 0.0001 | 0.0001 | KP998303 |
| sosp_ng291 | 1 | A | 4 | PET_ACAGCAGTGTGACCTCCCTC | gtttCTGACCGCTCTTCATTGTCA | 0.1 | 25 | 59 | 25 | 2457 | 1.00 | 2457 | 12 | 132-177 | 0.60 | 0.60 | 1.00 | 0.0002 | 0.0001 | KP998304 |
| sosp_ng303 | 1 | A | 4 | VIC_GAACTCAGCTGGGACAGGAA | gtttCTGTGACACTGCTGCTCCAT | 0.04 | 25 | 59 | 25 | 2458 | 1.00 | 2458 | 6 | 163-183 | 0.51 | 0.51 | 0.99 | 0.0002 | 0.0001 | KP998305 |
| sosp_ng329 | 1 | A | 3 | NED_GGTGAACCAGGAGGCAAATA | gtttcGGAAAGTCTCTGATGCAGGC | 0.06 | 25 | 59 | 25 | 2466 | 1.00 | 2457 | 4 | 238-244 | 0.34 | 0.33 | 0.99 | 0.0004 | 0.0001 | KP998306 |
| sosp_ng347 | 1 | A | 3 | PET_CCTCTGCTTGCAAATGAACA | gtttCACCACGACTTCTGTTGTGC | 0.04 | 25 | 59 | 25 | 2462 | 1.00 | 2462 | 3 | 209-221 | 0.50 | 0.50 | 1.01 | 0.0003 | 0.0002 | KP998307 |
| sosp_ng221 | 1 | A | 5 | NED_CCACCTTGGCTTTGTATGGT | gtttCCATCCAATCTCATGTCATCC | 0.2 | 26 | 59 | 25 | 2443 | 0.99 | 2414 | 24 | 99-188 | 0.86 | 0.88 | 1.02 | 0.0001 | 0.0009 | KP998308 |
| sosp_ng259 | 1 | A | 2 | FAM_GGCAGCAGTGACTTCAGAAA | gtttcGGGTTAAAGGTAGGCAGCCC | 0.14 | 26 | 59 | 25 | 2429 | 0.98 | 2429 | 5 | 104-116 | 0.46 | 0.47 | 1.01 | 0.0002 | 0.0001 | KP998309 |
| sosp_ng278 | 1 | A | 3 | VIC_GGTGTGGAGGTGAAAGTGCT | gtttcGCAAGGGTCTGTTGATGGAT | 0.04 | 26 | 59 | 25 | 2444 | 0.99 | 2440 | 20 | 150-221 | 0.78 | 0.80 | 1.03 | 0.0001 | 0.0005 | KP998310 |
| sosp_ng390 | 1 | A | 3 | FAM_AGCTTGTGTTGAAGACATCCAG | gtttcGCTGATGGCTTTGTGAGTGA | 0.06 | 26 | 59 | 25 | 2464 | 1.00 | 2464 | 4 | 257-269 | 0.54 | 0.54 | 0.99 | 0.0002 | 0.0001 | KP998311 |
| sosp_ng396 | 1 | A | 4 | VIC_TGATGAGTGACCAGACTGGATT | gtttcAGGTGCAGGTCTGCCAGTTA | 0.06 | 26 | 59 | 25 | 2443 | 0.99 | 2347 | 12 | 241-276 | 0.78 | 0.77 | 0.99 | 0.0012 | 0.0116 | KP998312 |
| sosp_ng040 | 1 | A | 5 | NED_ATATCCAGTGCAGGAATGGG | gtttcTGATGTGGCAAGAGATGTCC | 0.3 | 27 | 59 | 25 | 2375 | 0.96 | 2365 | 16 | 123-195 | 0.86 | 0.85 | 0.99 | 0.0005 | 0.0011 | KP998313 |
| sosp_ng203 | 1 | A | 5 | VIC_CACTGAGCCATGCAGGAAT | gtttcAAACACTGGTGCTGGAGAGG | 0.03 | 27 | 59 | 25 | 2465 | 1.00 | 2429 | 8 | 126-163 | 0.71 | 0.71 | 1.00 | 0.0118 | 0.0001 | KP998314 |
| sosp_ng257 | 1 | A | 4 | FAM_TATGAGAGGGTGGCCTGAAC | gtttCCTGATCTCAGGTTGCCTTG | 0.2 | 27 | 59 | 25 | 2315 | 0.94 | 2315 | 3 | 83-95 | 0.42 | 0.40 | 0.97 | 0.0003 | 0.0001 | KP998315 |
| sosp_ng296 | 1 | A | 4 | FAM_CCCTGAACCCTGTATTTCCC | gtttcAGACAGACTGGAGGAAGGCA | 0.2 | 27 | 59 | 25 | 2463 | 1.00 | 2463 | 6 | 137-163 | 0.70 | 0.70 | 0.99 | 0.0002 | 0.0001 | KP998316 |
| sosp_ng315 | 1 | A | 4 | PET_ATCTTCCATCTTGCCACCAC | gtttCAAGCAGGGTGTCACTGTGT | 0.24 | 27 | 59 | 25 | 2430 | 0.98 | 2416 | 11 | 125-167 | 0.79 | 0.79 | 1.01 | 0.0005 | 0.0012 | KP998317 |
| sosp_ng322 | 1 | A | 3 | VIC_CTGGATGCAGGAGATTGGTT | gtttcAGCAAATGTGACCTGAGGCT | 0.03 | 27 | 59 | 25 | 2462 | 1.00 | 2313 | 4 | 203-212 | 0.48 | 0.50 | 1.04 | 0.0480 | 0.0001 | KP998318 |
| sosp_ng369 | 1 | A | 3 | PET_TGCCCTGATTCTCATCCTTC | gttTCCTAGCATTTCCATCCCTG | 0.03 | 27 | 59 | 25 | 2452 | 0.99 | 2452 | 4 | 189-198 | 0.40 | 0.42 | 1.06 | 0.0003 | 0.0001 | KP998319 |
| sosp_ng378 | 1 | A | 3 | FAM_ACAGCTAAAGGCAGTGAGGG | gtttcAGGGCTCAGAGTTTCCACCT | 0.14 | 27 | 59 | 25 | 2463 | 1.00 | 2463 | 3 | 224-233 | 0.59 | 0.58 | 0.99 | 0.0002 | 0.0001 | KP998320 |
| sosp_ng213 | 1 | A | 3 | FAM_TGTTTCAAAGTCTTGCCGTG | gtttcATCCATTTCAGCCACAGGTC | 0.04 | 28 | 59 | 25 | 2444 | 0.99 | 2441 | 4 | 136-146 | 0.49 | 0.48 | 0.98 | 0.0003 | 0.0002 | KP998321 |
| sosp_ng222 | 1 | A | 3 | VIC_GGAATGATGGGCTATGGACA | gtttcAACAAAGGCAGAAATGGTCG | 0.03 | 28 | 59 | 25 | 2451 | 0.99 | 2451 | 4 | 131-144 | 0.29 | 0.29 | 0.98 | 0.0004 | 0.0001 | KP998322 |
| sosp_ng255 | 1 | A | 4 | NED_CCTCTGCCTGTCCTGTGTTT | gtttcTGCAAGGACTGCATGTGTCT | 0.3 | 28 | 59 | 25 | 2437 | 0.99 | 2375 | 19 | 129-173 | 0.89 | 0.89 | 1.00 | 0.0009 | 0.0070 | KP998323 |
| sosp_ng285 | 1 | A | 4 | PET_CATTTCAGGGCTTTGCAGTT | gttTCCAAATGGACTTTGTGGTG | 0.2 | 28 | 59 | 25 | 2431 | 0.98 | 2431 | 3 | 152-164 | 0.54 | 0.56 | 1.03 | 0.0002 | 0.0001 | KP998324 |
| sosp_ng341 | 1 | A | 3 | VIC_CAGGAGCAGGAGGTCAAACT | gtttCTCAGGTCTGCATACGAGCA | 0.03 | 28 | 59 | 25 | 2464 | 1.00 | 2464 | 5 | 190-202 | 0.59 | 0.58 | 0.98 | 0.0002 | 0.0001 | KP998325 |
| sosp_ng240 | 1 | A | 5 | NED_ACATGAGATGAGACCGCTCC | gtttcTGGCATTCATAACCTGTGTCA | 0.06 | 29 | 59 | 25 | 2452 | 0.99 | 2452 | 4 | 104-119 | 0.27 | 0.27 | 0.99 | 0.0005 | 0.0001 | KP998326 |
| sosp_ng246 | 1 | A | 4 | VIC_CATTGTCTGTCATCGAGCGT | gtttcTAAGAGGAGCCGAGTGGATG | 0.3 | 29 | 59 | 25 | 2361 | 0.96 | 2244 | 13 | 130-180 | 0.88 | 0.88 | 1.00 | 0.0002 | 0.0203 | KP998327 |
| sosp_ng249 | 1 | A | 5 | FAM_TTCCGTTATTGTGAACACCG | gtttCTGCCAGGAGCTGAGATGTT | 0.04 | 29 | 59 | 25 | 2455 | 0.99 | 2419 | 16 | 115-200 | 0.86 | 0.86 | 1.00 | 0.0001 | 0.0018 | KP998328 |
| sosp_ng289 | 1 | A | 4 | NED_GTTTGGAGAACCTTGGCTTG | gtttCCTTCCTTGTGGAAGCCTTT | 0.06 | 29 | 59 | 25 | 2458 | 1.00 | 2458 | 6 | 155-175 | 0.67 | 0.69 | 1.03 | 0.0002 | 0.0001 | KP998329 |
| sosp_ng302 | 1 | A | 4 | PET_TGCTCCTGCAGGTATGGAAT | gtttcGCCCAATCCAGAAGAACTCA | 0.06 | 29 | 59 | 25 | 2447 | 0.99 | 2443 | 10 | 97-164 | 0.74 | 0.74 | 1.00 | 0.0001 | 0.0001 | KP998330 |
| sosp_ng324 | 1 | A | 4 | VIC_TGGGTAAGAGGAATTACAGTGGA | gtttCCAAACAGGCATAATTGGGA | 0.2 | 29 | 59 | 25 | 2413 | 0.98 | 2293 | 17 | 219-262 | 0.88 | 0.86 | 0.98 | 0.0003 | 0.0154 | KP998331 |
| sosp_ng362 | 1 | A | 3 | NED_AAGTCATGCGTGAGGGATTC | gtttCCCTCCCTTCCTCTCATTTC | 0.03 | 29 | 59 | 25 | 2455 | 0.99 | 2455 | 4 | 206-216 | 0.49 | 0.50 | 1.01 | 0.0002 | 0.0001 | KP998332 |

| marker | sel | chr | rep | forward primer | reverse primer | pc | panel | $T_A$ | cyc | $N_1$ | pr | $N_2$ | $N_A$ | range | $H_O$ | $H_E$ | $H_E/H_O$ | drop | false | GenBank |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| sosp_ng102 | 1 | A | 4 | FAM_ACAACGGCCAGTCAGGATAG | gttTCAAACTCCCATCCTCAACC | 0.04 | 30 | 59 | 25 | 2468 | 1.00 | 2468 | 4 | 181-193 | 0.36 | 0.36 | 1.01 | 0.0004 | 0.0001 | KP998333 |
| sosp_ng217 | 1 | A | 5 | NED_CTGTGAGCAGCCACAAGGT | gtttcTGGGACTTCATCAGAAGGCT | 0.04 | 30 | 59 | 25 | 2458 | 1.00 | 2455 | 9 | 100-145 | 0.75 | 0.73 | 0.97 | 0.0001 | 0.0001 | KP998334 |
| sosp_ng260 | 1 | A | 4 | FAM_GGATGCTTGAAATGCTTGCT | gtttcGGTTAGCACCACACTCCCAT | 0.12 | 30 | 59 | 25 | 2439 | 0.99 | 2394 | 4 | 128-140 | 0.62 | 0.61 | 0.99 | 0.0002 | 0.0001 | KP998335 |
| sosp_ng272 | 1 | A | 4 | VIC_TTGTGGCATTTGCTACATGG | gtttCCCACCTTACCCTCCCTAAG | 0.04 | 30 | 59 | 25 | 2462 | 1.00 | 2462 | 10 | 128-166 | 0.84 | 0.85 | 1.01 | 0.0001 | 0.0001 | KP998336 |
| sosp_ng300 | 1 | A | 4 | PET_GTCAGGATGCCACAAACACA | gtttCTGGCGTCACAGACACATCT | 0.08 | 30 | 59 | 25 | 2455 | 0.99 | 2340 | 7 | 140-165 | 0.57 | 0.62 | 1.09 | 0.0048 | 0.0001 | KP998337 |
| sosp_ng359 | 1 | A | 3 | VIC_GCTCAGGACAGGCTCCTTCT | gtttCCAGATCCAACAGCACCAG | 0.08 | 30 | 59 | 25 | 2461 | 1.00 | 2442 | 7 | 195-219 | 0.64 | 0.64 | 1.01 | 0.0009 | 0.0001 | KP998338 |
| sosp_ng371 | 1 | A | 4 | PET_AGTGAGGTGCCAAGGAACTG | gttTCCTCTTCACTATGTTCCAAGTCA | 0.24 | 30 | 59 | 25 | 2464 | 1.00 | 2422 | 13 | 183-235 | 0.80 | 0.80 | 1.01 | 0.0001 | 0.0036 | KP998339 |
| sosp_ng373 | 1 | A | 3 | NED_CGTGAGGAGCAGCTCTGAGT | gttTCCATTGATGCCATTTCTGA | 0.04 | 30 | 59 | 25 | 2463 | 1.00 | 2425 | 7 | 183-218 | 0.70 | 0.69 | 0.99 | 0.0006 | 0.0006 | KP998340 |
| sosp_ng201 | 1 | A | 2 | PET_TGTTGCATGTGCATGTGTCT | gtttCCCACTTTGATGGACCTTAATC | 0.08 | 31 | 59 | 25 | 2465 | 1.00 | 2456 | 7 | 95-113 | 0.69 | 0.68 | 0.98 | 0.0002 | 0.0006 | KP998341 |
| sosp_ng241 | 1 | A | 4 | VIC_GTTCTCAAACCACAATGCCC | gtttCTGAACTGCAAGGGCTGAAT | 0.08 | 31 | 59 | 25 | 2445 | 0.99 | 2435 | 3 | 100-108 | 0.60 | 0.60 | 1.00 | 0.0005 | 0.0010 | KP998342 |
| sosp_ng252 | 1 | A | 4 | NED_CCTGTGCCGTGAGTATTCCT | gtttCCCAGAATTCCAAAGGGACT | 0.04 | 31 | 59 | 25 | 2461 | 1.00 | 2461 | 2 | 85-93 | 0.22 | 0.22 | 1.01 | 0.0007 | 0.0001 | KP998343 |
| sosp_ng286 | 1 | A | 4 | VIC_ATGGAAGGGAGCAGCACTAA | gtttcTGCACTTGGTCAATCCTCTG | 0.08 | 31 | 59 | 25 | 2465 | 1.00 | 2427 | 15 | 161-217 | 0.80 | 0.79 | 0.99 | 0.0001 | 0.0035 | KP998344 |
| sosp_ng317 | 1 | A | 3 | PET_GGGTCTGGAGTGAGAAACCA | gttTCTCACTGCCAACTCAAGGA | 0.1 | 31 | 59 | 25 | 2464 | 1.00 | 2464 | 5 | 152-167 | 0.69 | 0.67 | 0.98 | 0.0002 | 0.0001 | KP998345 |
| sosp_ng330 | 1 | A | 3 | NED_GTGCAGCTGTAACACAACCC | gtttCCTTTCCAGAGCGATCCAC | 0.08 | 31 | 59 | 25 | 2463 | 1.00 | 2460 | 4 | 227-236 | 0.50 | 0.50 | 1.00 | 0.0002 | 0.0001 | KP998346 |
| sosp_ng336 | 1 | A | 3 | PET_AAAGCCATTAAGCCTCCCTG | gtttcACATGGTGCCCAATTCTCAT | 0.04 | 31 | 59 | 25 | 2459 | 1.00 | 2459 | 3 | 231-237 | 0.42 | 0.44 | 1.06 | 0.0006 | 0.0001 | KP998347 |
| sosp_ng393 | 1 | A | 5 | FAM_AACAAAGGGCAGCGACAG | gtttCATCAAGCTGTGCCAGACTC | 0.08 | 31 | 59 | 25 | 2462 | 1.00 | 2455 | 9 | 246-286 | 0.76 | 0.79 | 1.04 | 0.0001 | 0.0011 | KP998348 |
| sosp_ng218 | 1 | A | 4 | NED_TGCAAAGCTATGAAGGAGGG | gtttCAACAGGTTTACATGCAGCG | 0.04 | 32 | 59 | 25 | 2465 | 1.00 | 2462 | 3 | 102-110 | 0.21 | 0.21 | 0.99 | 0.0007 | 0.0001 | KP998349 |
| sosp_ng227 | 1 | A | 3 | VIC_CCGGAATCCAGATCATCCTA | gtttcTGCAGGTGTGATCAAGGTCT | 0.1 | 32 | 59 | 25 | 2463 | 1.00 | 2461 | 14 | 95-143 | 0.79 | 0.79 | 0.99 | 0.0001 | 0.0001 | KP998350 |
| sosp_ng248 | 1 | A | 2 | FAM_TTTGCAAACCAGGCAGAGT | gtttcAATTGCTGAGGACAAGCAGG | 0.04 | 32 | 59 | 25 | 2459 | 1.00 | 2456 | 5 | 90-100 | 0.24 | 0.23 | 0.96 | 0.0006 | 0.0001 | KP998351 |
| sosp_ng268 | 1 | A | 3 | PET_GAGGCCTGTTGTCCTTTCAG | gtttcGGAGTTTGGAACACGGGTAA | 0.24 | 32 | 59 | 25 | 2457 | 1.00 | 2204 | 17 | 140-221 | 0.76 | 0.79 | 1.04 | 0.0457 | 0.0010 | KP998352 |
| sosp_ng299 | 1 | A | 4 | FAM_TCCTCTGCTTTAGTGCTGCC | gtTTCCCACTGCTCCTCTCAGT | 0.14 | 32 | 59 | 25 | 2465 | 1.00 | 2339 | 4 | 143-155 | 0.48 | 0.51 | 1.06 | 0.0246 | 0.0001 | KP998353 |
| Sosp111 | 0 | A | 2 | VIC_AAAGTGGCAATTTGTCCTCG | gtttcTTTCCCTGAACAGGCATCTC | 0.2 | 6 | 59 | 28 | 2243 | 0.91 | 1873 | 10 | 107-147 | 0.55 | 0.67 | 1.22 | 0.1222 | 0.0001 | KP998354 |
| Sosp144 | 0 | A | 4 | NED_GCCTTTCCTGCTGTCTTCAC | gtttcAAGAGCTGCTTTATTTTCTCACG | 0.28 | 6 | 59 | 28 | 2361 | 0.96 | 2039 | 11 | 415-454 | 0.76 | 0.80 | 1.05 | 0.0944 | 0.0269 | KP998355 |
| Sosp028 | 0 | A | 4 | FAM_ATCTTCTTCCTTCCTCCCCA | gttTCAAACATTCAACCAATGGC | 0.04 | 8 | 59 | 28 | 2195 | 0.89 | 1731 | 9 | 260-325 | 0.66 | 0.78 | 1.18 | 0.1043 | 0.0022 | KP998356 |
| Sosp046 | 0 | A | 4 | VIC_GAGAAGAAACCACAGCTGCC | gtttcTGCTTGACAAACCCACGTTA | 0.08 | 8 | 59 | 28 | 1970 | 0.80 | 1144 | 12 | 90-141 | 0.39 | 0.82 | 2.13 | 0.4376 | 0.0130 | KP998357 |
| Mme001 | 0 | A | 2 | PET_AGGAAAAGGGAGGGAGAGGGTG | gtttcGGGAGTGCAGAATGTGCAAATG | 0.08 | 9 | 59 | 28 | 1822 | 0.74 | 1794 | 9 | 146-171 | 0.68 | 0.69 | 1.02 | 0.0003 | 0.0054 | AF127376 |
| Sosp021 | 0 | A | 4 | NED_ATTTCAACAAGTTGCCAGCC | gtttCAAGTTTGCACACCTTCAGC | 0.06 | 9 | 59 | 28 | 2242 | 0.91 | 1866 | 46 | 251-430 | 0.91 | 0.93 | 1.02 | 0.0192 | 0.0620 | KP998358 |
| Sosp058 | 0 | A | 2 | FAM_GAATCAGCACAACCACCTCA | gtttcAGTCCTGCTCAGTTCAGGGA | 0.04 | 10 | 59 | 28 | 2379 | 0.96 | 2378 | 2 | 361-364 | 0.01 | 0.01 | 0.99 | 0.0728 | 0.0005 | KP998359 |
| Sosp040 | 0 | A | 3 | VIC_GCTCTGCATCAAAAATGGAA | gtttCTCCACTGGTTTCTAAGGGC | 0.08 | 11 | 60 | 28 | 2280 | 0.92 | 1993 | 19 | 251-309 | 0.74 | 0.75 | 1.02 | 0.0386 | 0.0633 | KP998360 |
| Sosp027 | 0 | A | 4 | FAM_CCTTCATGCAGGAGGTTCAT | gtttCCATGCTGTGCACTTTTCTG | 0.14 | 12 | 60 | 28 | 2428 | 0.98 | 2336 | 23 | 262-415 | 0.86 | 0.86 | 1.00 | 0.0001 | 0.0535 | KP998361 |
| Sosp039 | 0 | A | 3 | PET_AAAACCCCACCCTGTTATGA | gtttcAGGCGTGACATCATTCCTTC | 0.4 | 13 | 58 | 32 | 2030 | 0.82 | 1345 | 16 | 125-193 | 0.55 | 0.87 | 1.58 | 0.3284 | 0.0025 | KP998362 |
| Sosp064 | 0 | A | 3 | PET_TGGCATCCCATTTTCAATTT | gtttcGAGCAACAAGCCAGAGAACC | 0.2 | 13 | 58 | 32 | 2378 | 0.96 | 1957 | 14 | 237-285 | 0.79 | 0.82 | 1.04 | 0.0807 | 0.0744 | KP998363 |
| sosp_ng022 | 0 | A | 2 | PET_GGGCACCTACAGAGCAGAAG | gtttcAAGGAGGAAGGAATGGGAAA | 0.06 | 15 | 60 | 25 | 2360 | 0.96 | 2060 | 4 | 107-125 | 0.33 | 0.35 | 1.08 | 0.1663 | 0.0118 | KP998364 |
| sosp_ng068 | 0 | A | 4 | VIC_GTGCAGAGGGAATGTGGTTT | gtttcAGTGGGAAGGACAGAGGGTT | 0.06 | 15 | 60 | 25 | 2315 | 0.94 | 1649 | 8 | 112-162 | 0.44 | 0.60 | 1.38 | 0.3464 | 0.0206 | KP998365 |
| sosp_ng121 | 0 | A | 5 | PET_TCAACCCAAATCTGACTCCA | gtttcTACTGCTTACGCAGGTGCAG | 0.3 | 15 | 60 | 25 | 2197 | 0.89 | 1717 | 13 | 183-243 | 0.77 | 0.88 | 1.14 | 0.0928 | 0.0236 | KP998366 |
| sosp_ng105 | 0 | A | 5 | FAM_ATCTGTTCCAGTGCCTCACC | gtttcGGAGCGATGTAGTGACAGCA | 0.16 | 16 | 60 | 25 | 2358 | 0.96 | 1609 | 9 | 145-200 | 0.68 | 0.81 | 1.19 | 0.1817 | 0.0158 | KP998367 |
| sosp_ng024 | 0 | A | 2 | FAM_GGCTGTTGGTACCTATGGGA | gtttcTACAACTAGCACGCATGCAC | 0.16 | 17 | 60 | 25 | 2280 | 0.92 | 1971 | 9 | 84-122 | 0.76 | 0.78 | 1.03 | 0.0301 | 0.0508 | KP998368 |
| sosp_ng079 | 0 | A | 2 | FAM_AACAGGAAAGGAGGTGCTGA | gtttcATGGAGAATCCTTGCCCTCT | 0.1 | 17 | 60 | 25 | 2370 | 0.96 | 1887 | 4 | 151-157 | 0.43 | 0.55 | 1.26 | 0.1969 | 0.0007 | KP998369 |

| marker | sel | chr | rep | forward primer | reverse primer | pc | panel | $T_A$ | cyc | $N_1$ | pr | $N_2$ | $N_A$ | range | $H_O$ | $H_E$ | $H_E/H_O$ | drop | false | GenBank |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| sosp_ng127 | 0 | A | 4 | VIC_GCAGCAGGTAGGACACTTCA | gtttcGGTATGGCAGGACACAAAGG | 0.06 | 17 | 60 | 25 | 2325 | 0.94 | 1889 | 11 | 186-222 | 0.77 | 0.81 | 1.06 | 0.1230 | 0.0129 | KP998370 |
| sosp_ng023 | 0 | A | 2 | VIC_AACAACACATGGAACTGGAGG | gtttcTTTACCTTGCATGTCTGCCA | 0.24 | 18 | 60 | 25 | 1872 | 0.76 | 1247 | 9 | 109-136 | 0.53 | 0.80 | 1.52 | 0.3132 | 0.0099 | KP998371 |
| sosp_ng093 | 0 | A | 5 | VIC_TTTCCTTTGCCAAACTCCAC | gtttcGGCATCACATTGCATCACAT | 0.1 | 18 | 60 | 25 | 2230 | 0.90 | 1903 | 12 | 153-208 | 0.74 | 0.80 | 1.07 | 0.1209 | 0.0071 | KP998372 |
| sosp_ng136 | 0 | A | 4 | VIC_CCTTCTCGGAGTTTGTGCTC | gtttCTTCTCCTTGGGAATGCAAA | 0.16 | 19 | 60 | 25 | 1355 | 0.55 | 673 | 6 | 207-223 | 0.40 | 0.77 | 1.96 | 0.5839 | 0.1122 | KP998373 |
| sosp_ng198 | 0 | A | 4 | PET_TTAGGCATCTGGGTGCTTTC | gTTTCAATGACCAGCTCAGGA | 0.06 | 19 | 60 | 25 | 2327 | 0.94 | 2178 | 3 | 298-306 | 0.35 | 0.36 | 1.01 | 0.0974 | 0.0002 | KP998374 |
| sosp_ng042 | 0 | A | 4 | FAM_GAAGACAGCTGAGGAGGTGG | gtttcAAACGGAAGTTTGTGGCAAG | 0.34 | 20 | 60 | 25 | 2164 | 0.88 | 1770 | 5 | 118-134 | 0.36 | 0.47 | 1.30 | 0.2612 | 0.0002 | KP998375 |
| sosp_ng066 | 0 | A | 2 | PET_GTCATGGCTGGAGTAAGGGA | gtttcGCAACTGCTGTAACAACGTGA | 0.06 | 20 | 60 | 25 | 2378 | 0.96 | 2239 | 5 | 140-151 | 0.56 | 0.59 | 1.05 | 0.0708 | 0.0001 | KP998376 |
| sosp_ng074 | 0 | A | 6 | VIC_ACACTGAGGTCAGGATGGGA | gtttcGCTCGGTTGTGAACACAGAA | 0.04 | 20 | 60 | 25 | 2192 | 0.89 | 1628 | 6 | 123-161 | 0.44 | 0.62 | 1.41 | 0.2624 | 0.0002 | KP998377 |
| sosp_ng106 | 0 | A | 4 | FAM_CAGGATGTGCAACACCAAAC | gtttcGAAAGGCAACCACCATGATT | 0.1 | 20 | 60 | 25 | 2270 | 0.92 | 1322 | 2 | 187-191 | 0.10 | 0.46 | 4.53 | 0.7983 | 0.0007 | KP998378 |
| sosp_ng014 | 0 | A | 6 | PET_CAGGGTCAGGGTTAGAGCTG | gtttCCTTGGAGGCTGAAATGACT | 0.2 | 21 | 60 | 25 | 2334 | 0.95 | 2075 | 12 | 94-229 | 0.56 | 0.62 | 1.10 | 0.0795 | 0.0007 | KP998379 |
| sosp_ng167 | 0 | A | 6 | FAM_CCTGAGATGCTGTTTCCTGA | gtttcGCCTCTTGGGTATTGGATCA | 0.24 | 21 | 60 | 25 | 2064 | 0.84 | 1701 | 5 | 250-274 | 0.24 | 0.49 | 2.05 | 0.3073 | 0.0002 | KP998380 |
| sosp_ng169 | 0 | A | 4 | VIC_GATCTGGTGCCTTCTTGCTC | gtttCTTCATGCCCATCCCTCTAA | 0.1 | 21 | 60 | 25 | 2134 | 0.86 | 1465 | 10 | 245-277 | 0.34 | 0.53 | 1.55 | 0.3561 | 0.0168 | KP998381 |
| sosp_ng005 | 0 | A | 2 | NED_GGATTTCAGAGCTCCCAGC | gtttcTAAAGACCACGCTGCTCACA | 0.04 | 22 | 60 | 25 | 2186 | 0.89 | 1754 | 5 | 89-100 | 0.31 | 0.52 | 1.69 | 0.2443 | 0.0002 | KP998382 |
| sosp_ng340 | 0 | A | 3 | FAM_TCTCTGTTCCTGCCCTGACT | gtttcTGATGTGCTCATTAGGCAGC | 0.3 | 23 | 59 | 25 | 1830 | 0.74 | 1603 | 3 | 232-243 | 0.31 | 0.40 | 1.32 | 0.1656 | 0.0005 | KP998383 |
| sosp_ng384 | 0 | A | 5 | PET_CCAGTTCCTAAAGATACGTGATGA | gtttcAATGTCCTGCCTGGAATGAG | 0.16 | 23 | 59 | 25 | 2350 | 0.95 | 1897 | 7 | 256-287 | 0.68 | 0.78 | 1.14 | 0.1259 | 0.0042 | KP998384 |
| sosp_ng116 | 0 | A | 2 | FAM_CTGGAATGCCAGGAAACAGT | gtttCATCACCACCTTCCAAATCC | 0.3 | 26 | 59 | 25 | 2378 | 0.96 | 1984 | 5 | 189-197 | 0.44 | 0.56 | 1.28 | 0.2264 | 0.0032 | KP998385 |
| sosp_ng323 | 0 | A | 4 | VIC_ATCCCAGCAGGTTTATGTGG | gtttcGCCTTCTGTCTGTATCCTTCCT | 0.06 | 28 | 59 | 25 | 1951 | 0.79 | 1373 | 7 | 238-258 | 0.36 | 0.72 | 1.98 | 0.3180 | 0.0007 | KP998386 |
| sosp_ng395 | 0 | A | 5 | PET_CAAAGTTCTTTCTCTGTGCCC | gtttcGGACACTGGAGTCTGCAACA | 0.08 | 28 | 59 | 25 | 2452 | 0.99 | 2293 | 8 | 248-277 | 0.69 | 0.71 | 1.03 | 0.0877 | 0.0001 | KP998387 |
| sosp_ng349 | 0 | A | 3 | PET_ATTTGTCACCCACAACAGCA | gtttcGCAGCCTCATGTTCCTCACT | 0.04 | 29 | 59 | 25 | 2452 | 0.99 | 2251 | 8 | 188-218 | 0.70 | 0.72 | 1.04 | 0.0725 | 0.0001 | KP998388 |
| sosp_ng386 | 0 | A | 5 | NED_TGAACACTACACAAACATGCCA | gtttCATGGTCAATGCAACAAACC | 0.04 | 30 | 59 | 25 | 2366 | 0.96 | 1956 | 4 | 233-258 | 0.38 | 0.50 | 1.31 | 0.1364 | 0.0001 | KP998389 |
| sosp_ng274 | 0 | A | 4 | VIC_TTAAAGGGTTGGAGCACACC | gtttcGCTGAGTTTGATGGAGACCC | 0.04 | 32 | 59 | 25 | 2174 | 0.88 | 1538 | 6 | 174-194 | 0.51 | 0.75 | 1.46 | 0.2512 | 0.0018 | KP998390 |
| sosp_ng388 | 0 | A | 4 | VIC_CGAGGAAGAGACTACCATTTCA | gtttCTTGCCCTCTGATCATCCAT | 0.3 | 32 | 59 | 25 | 2340 | 0.95 | 1694 | 7 | 256-279 | 0.42 | 0.51 | 1.21 | 0.1540 | 0.0426 | KP998391 |
| Sosp071 | 0 | W | 2 | NED_CAGCTGAACTAGAGACGGGG | gtttcTAGAACTCACCCCTTGTGCC | 0.04 | 11 | 60 | 28 | 1189 | 0.48 | . | 1 | 253-253 | 0.00 | 0.00 | . | . | . | KP998392 |
| sosp_ng192 | 0 | W | 4 | PET_TGCAGTAGCACAATTTGGGT | gtttcGTGAGCCGCTTCTCGTTTAC | 0.26 | 21 | 60 | 25 | 1177 | 0.48 | . | 7 | 287-319 | 0.00 | 0.74 | . | . | 0.0002 | KP998393 |
| Mme007 | 1 | Z | 2 | PET_TGCGAGCCTTTCCAAGTTTG | gtttcAACCCCACATGAAACAGGTCAC | 0.06 | 11 | 60 | 28 | 2372 | 0.96 | 2361 | 14 | 112-144 | 0.34 | 0.67 | 1.98 | 0.0004 | 0.0002 | AF127381 |
| Sosp090 | 1 | Z | 2 | PET_AACGGTGACATGGCTGAACT | gtttcTTTGCCTGTGTTACGTGAGC | 0.06 | 12 | 60 | 28 | 2284 | 0.92 | 2177 | 10 | 113-156 | 0.40 | 0.81 | 2.01 | 0.0159 | 0.0002 | KP998394 |
| sosp_ng152 | 1 | Z | 4 | PET_GGCACAATCCTATGCAACAA | gtttcTGCTGGGAAAGCTACACTGA | 0.06 | 16 | 60 | 25 | 2397 | 0.97 | 2390 | 6 | 215-235 | 0.35 | 0.66 | 1.89 | 0.0004 | 0.0002 | KP998395 |
| sosp_ng195 | 1 | Z | 5 | VIC_CAGTCCTCATTTGTGCTGGA | gttTCAGGCAATTGGACAAGATG | 0.16 | 18 | 60 | 25 | 2208 | 0.89 | 2177 | 9 | 274-314 | 0.40 | 0.79 | 1.97 | 0.0007 | 0.0014 | KP998396 |
| sosp_ng141 | 1 | Z | 5 | NED_ATGGCCTTTAGAGATGGCCT | gtttcGAAACTTCCTGCAGCCTGTC | 0.06 | 19 | 60 | 25 | 2341 | 0.94 | 2323 | 11 | 183-245 | 0.40 | 0.79 | 1.99 | 0.0011 | 0.0002 | KP998397 |
| sosp_ng258 | 1 | Z | 2 | VIC_ACAGCTCGTCCCTTCCAAAT | gtttcAGGAGAAGGATGGAGCTCTG | 0.03 | 26 | 59 | 25 | 2463 | 1.00 | 2463 | 4 | 103-109 | 0.29 | 0.56 | 1.96 | 0.0004 | 0.0002 | KP998398 |
| sosp_ng381 | 1 | Z | 5 | NED_GCAGTCATGCTGAAGAAATCTG | gtttCCTTTAAGAAAGGCAATGGACA | 0.06 | 26 | 59 | 25 | 2441 | 0.99 | 2412 | 8 | 214-259 | 0.29 | 0.59 | 2.05 | 0.0005 | 0.0010 | KP998399 |
| sosp_ng332 | 0 | Z | 3 | FAM_CCATGAGATTCCCTCCTTCA | gTTTCCTGTGCTTCTGCATCA | 0.24 | 24 | 59 | 25 | 2345 | 0.95 | 2075 | 9 | 181-205 | 0.30 | 0.76 | 2.53 | 0.0672 | 0.0027 | KP998400 |
| CHD | 0 | ZW | . | GAGRAAYTGTGCRAAACAGG | PET_GAGAYKGAGTCACTATCAGATCCAG | 0.1 | sex | 60 | 28 | 3160 | . | . | 2 | 252-302 | . | . | . | . | . | . |

All markers with ng in the name were developed from 454 sequencing data, all others from cloning or published sources.

Loci with *sel*=1 are loci of high quality (successfully typed in >75% of genotyped individuals and locus-specific allelic dropout and false allele rates <5%) that were used for linkage map construction. *chr* indicates if loci are autosomal, Z-linked or W-linked (A, Z or W, respectively). ZW has homologs of different length on the W and Z chromosomes. *rep* is the length of the repetitive sequence in base pairs. Sequences of forward and reverse primers are given, with fluorescent labels (FAM, VIC, NED, or PET) at the 5' end separated from the main sequence by a '_'. PIG-tail bases (Brownstein *et al.* 1996) are given in lower case. *pc* concentration of each primer in final polymerase chain reaction (PCR) in µM; *panel* name of multiplex PCR panel, loci with identical panel names are amplified in the same multiplex PCR; $T_A$ PCR annealing temperature in °C; *cyc* number of PCR cycles; $N_1$ number of individuals that were successfully genotyped for this locus; *pr* proportion of indidviduals that were successfully genotyped at this locus, *i.e.* $N_1$ divided by the number of individuals for which a PCR at the respective locus was attempted, but not considering the individuals where less than 75% of loci amplified (see text for details); $N_2$ number of genotyped individuals after having masked problematic genotypes detected at the family level for autosomal and Z-linked loci (see text for details); number of alleles ($N_A$), allele size range in base pairs (*range*), mean observed heterozygosity ($H_O$), expected heterozygosity ($H_E$) (Nei 1987, equation 8.1) and the ratio of $H_E/H_O$ after having masked problematic genotypes detected at the family level for autosomal loci; genotyping error rates (*drop* for allelic dropout, and *false* for rate of wrongly assigned alleles) were detected from the pedigree using 700,000 Markov chain Monte Carlo iterations in *MasterBayes* (see text for details); *GenBank* accession numbers.

**Table S2:** The number of markers of song sparrow linkage groups that map to zebra finch linkage groups are shown. This is an alternative display of the data shown in Figure 1 (main text). Two loci mapped to different linkage groups in the two species (marked with an asterisk; see main text).

| | | **marker location in song sparrow (*Melospiza melodia*)** | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | **1** | **1A** | **2** | **3** | **4** | **4A** | **5** | **6** | **7** | **8** | **9** | **10** | **11** | **12** | **13** | **14** | **15** | **17** | **18** | **19** | **20** | **21** | **22** | **E22** | **23** | **24** | **25** | **26** | **27** | **28** | **Z** | **W** | **unlinked** | **unknown** |
| **marker location in zebra finch (*Taeniopygia guttata*)** | **1** | 18 | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 6 |
| | **1A** | . | 12 | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 1 |
| | **2** | . | . | 12 | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 1 | 6 |
| | **3** | . | . | . | 11 | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 5 |
| | **4** | . | . | . | . | 5 | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 1 | 3 |
| | **4A** | . | . | . | . | . | 4 | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . |
| | **5** | . | . | . | . | . | . | 8 | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 1 |
| | **6** | . | . | . | . | . | . | . | 6 | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 2 |
| | **7** | . | . | . | . | . | . | . | . | 3 | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 1 | . |
| | **8** | . | . | . | . | . | . | . | . | . | 3 | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . |
| | **9** | . | . | . | . | . | . | . | . | . | . | 8 | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 1 |
| | **10** | . | . | . | . | . | . | . | . | . | . | . | 2 | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 1 |
| | **11** | . | . | . | . | . | . | . | . | . | . | . | . | 2 | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . |
| | **12** | . | . | . | . | . | . | . | . | . | . | . | . | . | 2 | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . |
| | **13** | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 1 | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 1 |
| | **14** | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 2 | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 1 | 1 |
| | **15** | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 2 | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 1 |
| | **17** | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 3 | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 1 |
| | **18** | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 4 | . | . | . | . | . | . | . | . | . | . | . | . | . | . |
| | **19** | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 2 | . | . | . | . | . | . | . | . | . | . | . | 1 | 1 |
| | **20** | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 2 | . | . | . | . | . | . | . | . | . | . | . | . |
| | **21** | . | . | . | . | 2* | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . |
| | **22** | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 1 | . | . | . | . | . | . | . | . | . | . |
| | **E22** | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 1 | . | . | . | . | . | . | . | . | . | . |
| | **23** | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 2 | . | . | . | . | . | . | . | . | . |
| | **24** | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 3 | . | . | . | . | . | . | . | 2 |
| | **25** | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 2 | . | . | . | . | . | . | . |
| | **26** | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 5 | . | . | . | . | . | . |
| | **27** | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 4 | . | . | . | . | . |
| | **28** | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 1 |
| | **Z** | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | 7 | . | . | . |
| | **unknown** | 2 | . | 1 | 1 | 3 | 1 | 1 | 2 | . | 1 | 1 | . | 2 | 1 | . | . | . | 1 | 1 | . | . | . | . | . | 1 | . | . | 2 | . | 1 | 2 | 2 | 5 |

*unlinked* = markers that were not linked to any other markers in the linkage analysis for song sparrows; *unknown* = markers that could not be mapped to a linkage group

**Table S3:** Linkage map statistics, with marker mapping locations in the zebra finch (*Taeniopygia guttata*) and song sparrow (*Melospiza melodia*) genomes, as well as the number of (informative) meiosis events available for song sparrow linkage mapping. This table is sorted by marker name.

| Marker | *T.g.* LG | *T.g.* loc. (kbp) | *M.m.* LG | *M.m.* av. loc. (cM) | *M.m.* fem. loc. (cM) | *M.m.* m. loc. (cM) | meiosis | inf. meiosis |
|---|---|---|---|---|---|---|---|---|
| Escμ001 | . | . | 2 | 25.2 | 19.1 | 32.6 | 1821 | 1250 |
| Gf005 | 1A | 52,065 | 1A | 42.1 | 41.6 | 42.9 | 1660 | 1278 |
| Mme001 | 19 | 1,726 | . | . | . | . | . | . |
| Mme002 | 3 | 9,301 | 3 | 121.0 | 121.4 | 123.9 | 1782 | 1323 |
| Mme007 | Z | 9,152 | Z | 0.0 | 0.0 | 0.0 | 1891 | 1536 |
| Mme008 | 10 | 15,087 | 10 | 0.0 | 0.0 | 0.0 | 1995 | 1500 |
| Mme012 | . | . | 1 | 133.4 | 126.3 | 141.7 | 1247 | 720 |
| sosp_ng001 | 11 | 10,794 | 11 | 3.8 | 2.3 | 5.3 | 1769 | 1302 |
| sosp_ng002 | 5 | 26,989 | 5 | 125.1 | 134.5 | 116.5 | 1020 | 347 |
| sosp_ng004 | . | . | 9 | 9.2 | 8.0 | 10.5 | 1014 | 662 |
| sosp_ng005 | . | . | . | . | . | . | . | . |
| sosp_ng006 | 2 | 40,678 | 2 | 126.5 | 112.1 | 144.9 | 958 | 431 |
| sosp_ng007 | 1 | 5,228 | 1 | 183.9 | 177.2 | 192.3 | 929 | 370 |
| sosp_ng008 | 1 | 104,745 | 1 | 26.1 | 26.5 | 25.9 | 1604 | 1153 |
| sosp_ng012 | 5 | 37,370 | 5 | 49.6 | 56.4 | 43.7 | 1650 | 944 |
| sosp_ng014 | 28 | . | . | . | . | . | . | . |
| sosp_ng022 | 1 | 5,568 | . | . | . | . | . | . |
| sosp_ng023 | 4 | 17,925 | . | . | . | . | . | . |
| sosp_ng024 | 1 | 95,565 | . | . | . | . | . | . |
| sosp_ng033 | 1 | 101,819 | 1 | 14.7 | 12.4 | 17.0 | 1643 | 1021 |
| sosp_ng034 | 4 | 65,269 | unlinked | 0.0 | 0.0 | 0.0 | 1472 | 1054 |
| sosp_ng037 | . | . | unlinked | 0.0 | 0.0 | 0.0 | 1561 | 1088 |
| sosp_ng040 | . | . | 11 | 0.0 | 0.0 | 0.0 | 1893 | 1344 |
| sosp_ng042 | 15 | 5,683 | . | . | . | . | . | . |
| sosp_ng045 | 3 | 26,523 | 3 | 154.3 | 153.8 | 157.4 | 1034 | 550 |
| sosp_ng048 | 3 | 90,650 | 3 | 0.0 | 0.0 | 0.0 | 1446 | 923 |
| sosp_ng053 | 24 | 4,846 | 24 | 48.7 | 48.4 | 48.0 | 596 | 325 |
| sosp_ng054 | 1A | 25,107 | 1A | 87.7 | 81.1 | 94.6 | 1756 | 1333 |
| sosp_ng055 | 1 | 47,408 | 1 | 113.8 | 110.1 | 118.2 | 1502 | 1030 |
| sosp_ng058 | 5 | 6,774 | 5 | 66.8 | 73.6 | 60.9 | 1857 | 1298 |
| sosp_ng066 | 3 | 101,803 | . | . | . | . | . | . |
| sosp_ng068 | 24 | 6,117 | . | . | . | . | . | . |
| sosp_ng071 | . | . | 3 | 47.2 | 56.0 | 38.9 | 1939 | 1461 |
| sosp_ng072 | 2 | 35,164 | 2 | 143.4 | 122.6 | 167.9 | 1118 | 710 |
| sosp_ng074 | 13 | 15,944 | . | . | . | . | . | . |
| sosp_ng079 | 17 | 6,498 | . | . | . | . | . | . |
| sosp_ng081 | 15 | 14,300 | 15 | 0.0 | 0.0 | 0.0 | 1633 | 1149 |
| sosp_ng082 | 25 | 197 | 25 | 0.0 | 0.0 | 0.0 | 1557 | 1111 |
| sosp_ng083 | 3 | 25,901 | 3 | 148.8 | 150.6 | 150.5 | 679 | 485 |
| sosp_ng086 | 24 | 434 | 24 | 0.0 | 0.0 | 0.0 | 1455 | 1129 |
| sosp_ng088 | 18 | 2,502 | 18 | 17.4 | 9.3 | 24.8 | 1619 | 1097 |
| sosp_ng091 | 14 | 8,651 | unlinked | 0.0 | 0.0 | 0.0 | 687 | 463 |
| sosp_ng093 | 1 | 64,888 | . | . | . | . | . | . |
| sosp_ng096 | 4A | 14,174 | 4A | 11.5 | 11.9 | 11.4 | 216 | 72 |
| sosp_ng098 | 26 | 3,880 | 26 | 50.5 | 48.6 | 51.8 | 1336 | 816 |
| sosp_ng102 | 2 | 120,461 | 2 | 50.8 | 46.4 | 57.1 | 982 | 605 |
| sosp_ng105 | 6 | 11,652 | . | . | . | . | . | . |
| sosp_ng106 | 3 | 96,893 | . | . | . | . | . | . |

| Marker | *T.g.* LG | *T.g.* loc. (kbp) | *M.m.* LG | *M.m.* av. loc. (cM) | *M.m.* fem. loc. (cM) | *M.m.* m. loc. (cM) | meiosis | inf. meiosis |
|---|---|---|---|---|---|---|---|---|
| sosp_ng107 | 26 | 1,076 | 26 | 11.9 | 14.1 | 10.0 | 1584 | 862 |
| sosp_ng109 | 6 | 34,913 | 6 | 116.1 | 113.3 | 118.2 | 248 | 190 |
| sosp_ng113 | 14 | 1,022 | 14 | 0.0 | 0.0 | 0.0 | 1385 | 835 |
| sosp_ng115 | 27 | 280 | 27 | 10.6 | 4.2 | 16.5 | 337 | 263 |
| sosp_ng116 | 6 | 3,368 | . | . | . | . | . | . |
| sosp_ng119 | 4 | 61,459 | 4 | 4.1 | 5.2 | 3.7 | 1105 | 339 |
| sosp_ng120 | 3 | 85,387 | 3 | 160.2 | 161.3 | 162.3 | 1309 | 788 |
| sosp_ng121 | . | . | . | . | . | . | . | . |
| sosp_ng123 | . | . | 1 | 43.7 | 40.1 | 47.3 | 1286 | 839 |
| sosp_ng126 | 26 | 1,544 | 26 | 1.0 | 1.0 | 0.9 | 1860 | 1426 |
| sosp_ng127 | 3 | 97,535 | . | . | . | . | . | . |
| sosp_ng128 | 18 | 3,982 | 18 | 59.6 | 72.3 | 55.8 | 1408 | 909 |
| sosp_ng132 | 5 | 22,341 | 5 | 101.0 | 106.2 | 96.9 | 701 | 226 |
| sosp_ng134 | 17 | 8,223 | 17 | 1.1 | 1.0 | 1.2 | 1193 | 260 |
| sosp_ng136 | 24 | . | . | . | . | . | . | . |
| sosp_ng137 | . | . | 27 | 0.0 | 0.0 | 0.0 | 1743 | 1272 |
| sosp_ng141 | Z | 72,634 | Z | 57.7 | 0.0 | 240.5 | 1801 | 1387 |
| sosp_ng142 | . | . | 6 | 0.0 | 0.0 | 0.0 | 478 | 252 |
| sosp_ng146 | 1 | 98,072 | 1 | 0.1 | 0.0 | 0.3 | 1813 | 1376 |
| sosp_ng149 | 7 | 10,167 | 7 | 0.0 | 0.0 | 0.0 | 1738 | 1113 |
| sosp_ng152 | Z | 107 | Z | 39.1 | 0.0 | 144.6 | 1853 | 1472 |
| sosp_ng154 | 17 | 1,759 | 17 | 39.8 | 43.0 | 35.6 | 1275 | 769 |
| sosp_ng159 | 19 | 10,368 | 19 | 0.0 | 0.0 | 0.0 | 2092 | 1675 |
| sosp_ng160 | 9 | 22,763 | 9 | 61.7 | 63.3 | 60.6 | 1018 | 577 |
| sosp_ng161 | 6 | 3,123 | 6 | 27.0 | 13.9 | 36.3 | 563 | 366 |
| sosp_ng163 | 1 | 33,477 | 1 | 61.2 | 61.1 | 61.9 | 1426 | 961 |
| sosp_ng167 | 4 | 67,372 | . | . | . | . | . | . |
| sosp_ng169 | 3 | 81,488 | . | . | . | . | . | . |
| sosp_ng172 | 4 | 27,623 | 4 | 40.7 | 40.4 | 41.0 | 1892 | 1462 |
| sosp_ng173 | 1 | 97,826 | 1 | 0.0 | 0.0 | 0.0 | 1653 | 1052 |
| sosp_ng192 | . | . | W | . | . | . | . | . |
| sosp_ng194 | . | . | 8 | 52.1 | 58.3 | 48.1 | 1477 | 884 |
| sosp_ng195 | Z | 19,995 | Z | 19.3 | 0.0 | 48.5 | 1924 | 1526 |
| sosp_ng197 | . | . | 18 | 2.2 | 0.2 | 4.0 | 1861 | 1468 |
| sosp_ng198 | 14 | 8,352 | . | . | . | . | . | . |
| sosp_ng200 | 9 | 1,160 | 9 | 6.8 | 5.4 | 8.1 | 1591 | 1089 |
| sosp_ng201 | 1 | 30,892 | 1 | 57.2 | 56.4 | 58.5 | 1493 | 887 |
| sosp_ng203 | 24 | 1,185 | 24 | 4.3 | 0.3 | 8.2 | 1560 | 1017 |
| sosp_ng206 | 4 | 63,749 | 4 | 0.0 | 0.0 | 0.0 | 1642 | 1140 |
| sosp_ng213 | 1 | 74,288 | 1 | 117.0 | 114.0 | 120.8 | 1179 | 342 |
| sosp_ng215 | 2 | 30,966 | 2 | 140.0 | 120.4 | 163.9 | 1581 | 981 |
| sosp_ng217 | . | . | 4 | 11.6 | 10.6 | 12.7 | 1591 | 1057 |
| sosp_ng218 | 6 | 36,033 | 6 | 121.6 | 114.0 | 132.4 | 513 | 286 |
| sosp_ng219 | 2 | 77,446 | 2 | 143.2 | 122.6 | 167.7 | 1359 | 918 |
| sosp_ng221 | . | . | 17 | 0.0 | 0.0 | 0.0 | 2003 | 1567 |
| sosp_ng222 | 23 | . | 23 | 0.0 | 0.0 | 0.0 | 658 | 424 |
| sosp_ng227 | 12 | 261 | 12 | 69.1 | 73.3 | 65.2 | 1757 | 1256 |
| sosp_ng238 | . | . | 27 | 8.3 | 3.6 | 12.5 | 1954 | 1511 |
| sosp_ng239 | 13 | 9,607 | unlinked | 0.0 | 0.0 | 0.0 | 657 | 450 |
| sosp_ng240 | 3 | 70,035 | 3 | 40.5 | 50.0 | 31.6 | 544 | 387 |
| sosp_ng241 | 1 | 91,350 | 1 | 141.4 | 130.8 | 154.1 | 1229 | 625 |
| sosp_ng246 | 1A | 3,602 | 1A | 0.0 | 0.0 | 0.0 | 1655 | 1144 |
| sosp_ng247 | . | . | 6 | 53.5 | 43.4 | 60.8 | 1270 | 603 |
| sosp_ng248 | 8 | . | 8 | 43.8 | 54.5 | 28.2 | 612 | 428 |
| sosp_ng249 | 21 | 3,126 | 4 | 146.5 | 148.9 | 143.9 | 1870 | 1403 |

| Marker | *T.g.* LG | *T.g.* loc. (kbp) | *M.m.* LG | *M.m.* av. loc. (cM) | *M.m.* fem. loc. (cM) | *M.m.* m. loc. (cM) | meiosis | inf. meiosis |
|---|---|---|---|---|---|---|---|---|
| sosp_ng252 | 9 | 25,788 | 9 | 79.3 | 73.6 | 83.7 | 534 | 252 |
| sosp_ng255 | 6 | 23,537 | 6 | 70.2 | 61.9 | 75.7 | 1837 | 1390 |
| sosp_ng256 | 1 | 29,611 | 1 | 55.0 | 54.0 | 56.5 | 1526 | 936 |
| sosp_ng257 | 2 | 22,223 | unlinked | 0.0 | 0.0 | 0.0 | 776 | 291 |
| sosp_ng258 | Z | 32,371 | Z | 38.9 | 0.0 | 144.1 | 1740 | 1394 |
| sosp_ng259 | 18 | 1,891 | 18 | 0.0 | 0.0 | 0.0 | 1289 | 837 |
| sosp_ng260 | 3 | 37,087 | 3 | 94.5 | 96.2 | 96.0 | 1250 | 777 |
| sosp_ng268 | 1 | 1,422 | 1 | 203.1 | 198.6 | 210.1 | 1363 | 912 |
| sosp_ng269 | . | . | 11 | 2.7 | 1.6 | 3.8 | 1645 | 1104 |
| sosp_ng272 | 5 | 7,819 | 5 | 68.3 | 75.3 | 62.1 | 1849 | 1455 |
| sosp_ng274 | 2 | 151,970 | . | . | . | . | . | . |
| sosp_ng278 | 2 | 156,119 | 2 | 0.0 | 0.0 | 0.0 | 1843 | 1410 |
| sosp_ng279 | 6 | 34,313 | 6 | 114.4 | 113.3 | 113.4 | 1804 | 1193 |
| sosp_ng285 | 7 | 4 | unlinked | 0.0 | 0.0 | 0.0 | 1339 | 721 |
| sosp_ng286 | 4A | 8,051 | 4A | 2.2 | 1.9 | 2.5 | 1788 | 1237 |
| sosp_ng289 | 4 | 27,056 | 4 | 39.9 | 39.5 | 40.3 | 1713 | 1131 |
| sosp_ng291 | 1 | 113,778 | 1 | 149.7 | 138.4 | 162.8 | 1419 | 894 |
| sosp_ng296 | . | . | 4 | 121.1 | 120.5 | 121.7 | 1256 | 706 |
| sosp_ng299 | 14 | 3,098 | 14 | 10.2 | 15.8 | 5.2 | 1108 | 641 |
| sosp_ng300 | 1A | 14,928 | 1A | 101.1 | 97.6 | 105.3 | 1112 | 786 |
| sosp_ng302 | . | . | 5 | 121.5 | 130.7 | 113.4 | 1665 | 1187 |
| sosp_ng303 | 26 | 1,790 | 26 | 0.0 | 0.0 | 0.0 | 1124 | 752 |
| sosp_ng315 | 10 | 2,793 | 10 | 39.8 | 54.0 | 30.1 | 1816 | 1344 |
| sosp_ng317 | 1A | 46,627 | 1A | 49.6 | 47.6 | 51.8 | 1514 | 681 |
| sosp_ng322 | 20 | 1,943 | 20 | 19.7 | 24.9 | 12.9 | 1247 | 769 |
| sosp_ng323 | . | . | . | . | . | . | . | . |
| sosp_ng324 | 4A | 6,777 | 4A | 0.0 | 0.0 | 0.0 | 1809 | 1383 |
| sosp_ng329 | 4A | 9,375 | 4A | 3.8 | 3.9 | 3.6 | 834 | 339 |
| sosp_ng330 | 19 | 8,827 | 19 | 7.9 | 4.5 | 11.6 | 1233 | 588 |
| sosp_ng332 | Z | 72,160 | Z | . | . | . | . | . |
| sosp_ng334 | 27 | . | 27 | 48.4 | 48.0 | 48.0 | 1106 | 290 |
| sosp_ng336 | 19 | 1,211 | unlinked | 0.0 | 0.0 | 0.0 | 584 | 258 |
| sosp_ng340 | 9 | 9,552 | . | . | . | . | . | . |
| sosp_ng341 | 1 | 12,339 | 1 | 164.6 | 154.4 | 176.5 | 1187 | 433 |
| sosp_ng343 | 3 | 20,655 | 3 | 124.5 | 125.0 | 127.7 | 1005 | 572 |
| sosp_ng347 | 8 | 18,295 | 8 | 0.0 | 0.0 | 0.0 | 1151 | 286 |
| sosp_ng349 | 4 | 44,749 | . | . | . | . | . | . |
| sosp_ng351 | 9 | 4,810 | 9 | 17.2 | 14.8 | 19.1 | 487 | 202 |
| sosp_ng358 | 1A | 70,379 | 1A | 22.4 | 18.8 | 26.0 | 543 | 402 |
| sosp_ng359 | 17 | 3,950 | 17 | 24.4 | 23.9 | 25.5 | 1532 | 1085 |
| sosp_ng362 | E22 | 178 | unlinked | 0.0 | 0.0 | 0.0 | 1206 | 647 |
| sosp_ng369 | 15 | 13,799 | 15 | 0.2 | 0.0 | 0.4 | 1294 | 600 |
| sosp_ng371 | 1 | 30,024 | 1 | 56.2 | 55.2 | 57.8 | 1701 | 1177 |
| sosp_ng373 | . | . | 24 | 18.3 | 7.5 | 27.9 | 1423 | 709 |
| sosp_ng378 | 27 | 2,643 | 27 | 39.8 | 36.7 | 42.4 | 1293 | 792 |
| sosp_ng381 | Z | 64,396 | Z | 9.9 | 0.0 | 26.3 | 1715 | 1364 |
| sosp_ng384 | 3 | 73,098 | . | . | . | . | . | . |
| sosp_ng385 | . | . | unlinked | 0.0 | 0.0 | 0.0 | 873 | 455 |
| sosp_ng386 | 1 | 64,131 | . | . | . | . | . | . |
| sosp_ng388 | 1 | 57,310 | . | . | . | . | . | . |
| sosp_ng390 | 9 | 4,233 | 9 | 19.4 | 17.8 | 21.0 | 1266 | 807 |
| sosp_ng392 | 2 | 144,065 | 2 | 21.7 | 16.1 | 28.5 | 1475 | 737 |
| sosp_ng393 | . | . | 4A | 27.8 | 32.1 | 23.3 | 1734 | 1015 |
| sosp_ng395 | 1A | 8,188 | . | . | . | . | . | . |
| sosp_ng396 | 21 | 1,322 | 4 | 131.6 | 132.4 | 130.7 | 1594 | 1084 |

| Marker | *T.g.* LG | *T.g.* loc. (kbp) | *M.m.* LG | *M.m.* av. loc. (cM) | *M.m.* fem. loc. (cM) | *M.m.* m. loc. (cM) | meiosis | inf. meiosis |
|---|---|---|---|---|---|---|---|---|
| Sosp001 | 27 | 3,328 | 27 | 54.7 | 56.8 | 51.4 | 1815 | 1322 |
| Sosp002 | 7 | 1,230 | 7 | 71.0 | 66.6 | 76.1 | 1689 | 1123 |
| Sosp003 | 9 | 3,983 | 9 | 0.0 | 0.0 | 0.0 | 1892 | 1421 |
| Sosp004 | 25 | . | 25 | 17.4 | 21.9 | 13.8 | 1403 | 928 |
| Sosp005 | 26 | . | 26 | 56.0 | 48.6 | 63.1 | 1442 | 848 |
| Sosp007 | 6 | 11,471 | 6 | 64.7 | 54.1 | 72.2 | 1293 | 399 |
| Sosp008 | 23 | 1,680 | 23 | 32.5 | 47.2 | 20.1 | 339 | 227 |
| Sosp010 | 1A | 52,890 | 1A | 41.4 | 41.2 | 41.9 | 1379 | 666 |
| Sosp012 | 9 | 19,106 | 9 | 48.2 | 52.2 | 44.7 | 1712 | 1288 |
| Sosp013 | 11 | 12,997 | 11 | 41.8 | 39.9 | 43.6 | 1786 | 1199 |
| Sosp014 | . | . | 4 | 126.9 | 126.8 | 127.1 | 1423 | 951 |
| Sosp017 | 1A | 52,226 | 1A | 41.7 | 41.2 | 42.6 | 1554 | 1069 |
| Sosp018 | 12 | 10,437 | 12 | 3.2 | 4.6 | 1.8 | 1215 | 596 |
| Sosp021 | 2 | 132,899 | . | . | . | . | . | . |
| Sosp022 | 5 | 5,822 | 5 | 65.3 | 72.4 | 59.1 | 1947 | 1507 |
| Sosp024 | 2 | 99,470 | 2 | 92.7 | 87.0 | 100.1 | 1509 | 1139 |
| Sosp025 | 2 | 142,832 | 2 | 25.5 | 19.7 | 32.6 | 1726 | 1303 |
| Sosp027 | 1 | 71,110 | . | . | . | . | . | . |
| Sosp028 | 2 | 136,170 | . | . | . | . | . | . |
| Sosp029 | 2 | 31,434 | 2 | 140.8 | 121.1 | 164.9 | 1678 | 1067 |
| Sosp030 | 8 | 14,640 | 8 | 5.6 | 7.1 | 4.2 | 1924 | 1420 |
| Sosp033 | 5 | 20,329 | 5 | 92.9 | 96.8 | 90.1 | 1644 | 1121 |
| Sosp035 | 1 | 65,949 | 1 | 89.1 | 88.9 | 90.1 | 1483 | 838 |
| Sosp037 | 22 | . | unlinked | 0.0 | 0.0 | 0.0 | 1418 | 855 |
| Sosp039 | . | . | . | . | . | . | . | . |
| Sosp040 | 5 | 45,272 | . | . | . | . | . | . |
| Sosp041 | 1A | 27,712 | 1A | 84.8 | 77.9 | 92.0 | 1263 | 809 |
| Sosp043 | 9 | 16,284 | 9 | 42.7 | 43.7 | 42.2 | 1689 | 1188 |
| Sosp046 | 2 | 127,766 | . | . | . | . | . | . |
| Sosp047 | 2 | 33,995 | 2 | 145.3 | 126.5 | 169.0 | 1040 | 627 |
| Sosp049 | 5 | 57,791 | 5 | 0.0 | 0.0 | 0.0 | 1316 | 678 |
| Sosp050 | 1A | 50,368 | 1A | 44.3 | 43.4 | 45.4 | 1860 | 1389 |
| Sosp052 | 1 | 62,605 | 1 | 94.3 | 92.7 | 96.6 | 1593 | 1105 |
| Sosp054 | 7 | 22,722 | 7 | 10.8 | 10.8 | 10.8 | 1567 | 1150 |
| Sosp055 | 3 | 13,160 | 3 | 115.7 | 117.8 | 117.1 | 1429 | 902 |
| Sosp056 | 3 | 8,947 | 3 | 121.1 | 121.4 | 124.1 | 1091 | 642 |
| Sosp058 | 2 | 53,659 | . | . | . | . | . | . |
| Sosp061 | 1A | 70,380 | 1A | 22.4 | 18.8 | 26.0 | 1857 | 1421 |
| Sosp062 | . | . | 12 | 0.0 | 0.0 | 0.0 | 1853 | 1405 |
| Sosp064 | 10 | 1,593 | . | . | . | . | . | . |
| Sosp065 | 18 | 4,059 | 18 | 59.7 | 72.4 | 55.8 | 1546 | 1059 |
| Sosp068 | 20 | 5,801 | 20 | 0.0 | 0.0 | 0.0 | 1557 | 1047 |
| Sosp069 | 1 | 91,608 | 1 | 141.7 | 130.9 | 154.4 | 1642 | 1145 |
| Sosp070 | 3 | 99,766 | 3 | 28.6 | 31.7 | 26.5 | 666 | 437 |
| Sosp071 | . | . | W | . | . | . | . | . |
| Sosp076 | 1A | 14,688 | 1A | 102.0 | 98.0 | 106.7 | 1693 | 1249 |
| Sosp090 | . | . | Z | 16.8 | 0.0 | 43.1 | 1896 | 1522 |
| Sosp111 | . | . | . | . | . | . | . | . |
| Sosp141 | 4 | 27,564 | 4 | 40.6 | 40.3 | 40.9 | 1517 | 888 |
| Sosp142 | 2 | 35,173 | 2 | 143.6 | 122.6 | 168.1 | 994 | 469 |
| Sosp144 | 2 | 126,894 | . | . | . | . | . | . |

Locations of markers on zebra finch (*T.g.* LG) and song sparrow (*M.m.* LG) linkage groups in units of 1000 base pairs (kbp, *T.g.* loc), or centiMorgans (cM) for the sex-averaged (*M.m.* av. loc.), female (*M.m.* fem. loc.), and male

(*M.m.* m. loc.) song sparrow linkage maps, respectively. *Meiosis* and *inf. meiosis* list the number of meiosis and phase-known (informative) meiosis events for all markers used in linkage map construction in song sparrows.

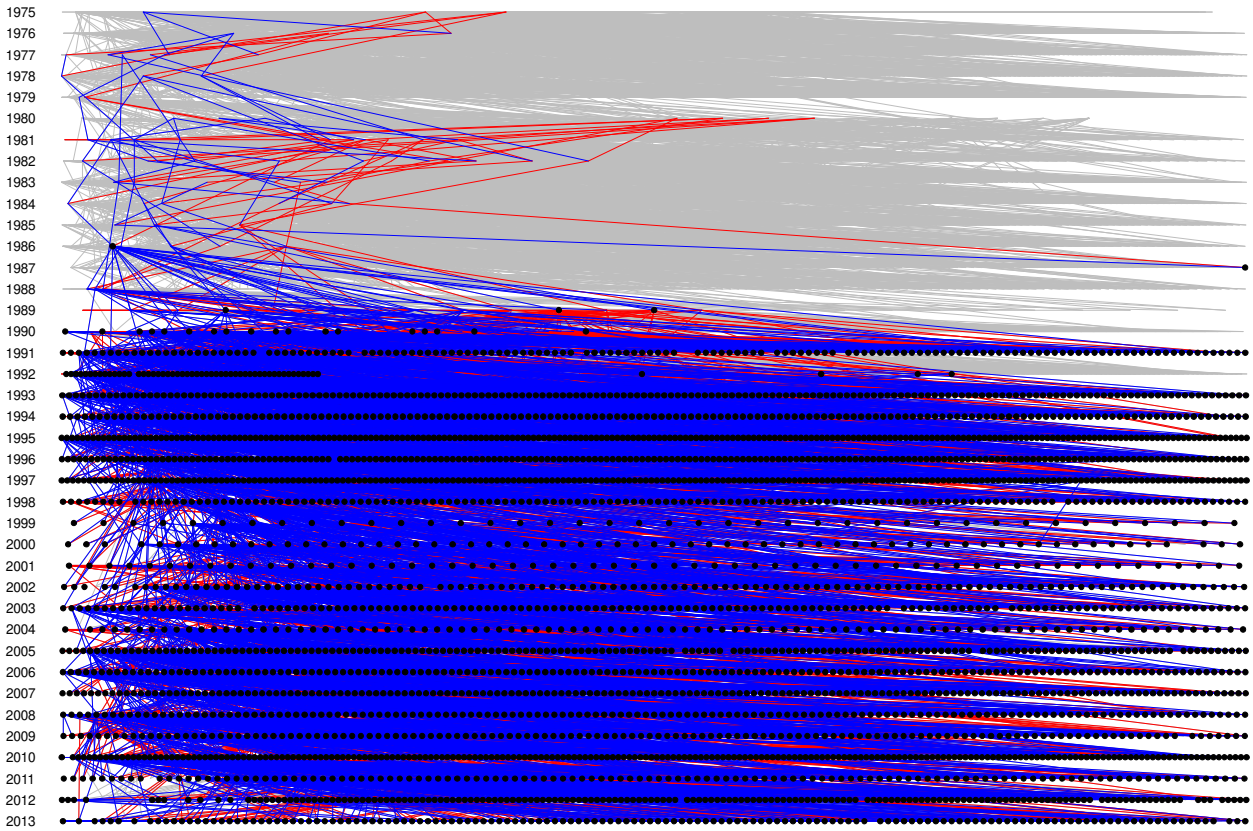


**Figure S1:** Pedigree of song sparrows from Mandarte Island. Black dots mark genetically sampled individuals and lines connect individuals to their mothers (blue and grey lines) and fathers (red and grey lines). Only those pedigree links that are informative about relatedness of genetically sampled individuals are printed in blue or red; the other pedigree links are printed in grey. The pedigree is sorted according to year of hatching.